Product and Method

The present invention relates to oligonucleotide probes, for use in assessing gene transcript levels in a cell, which may be used in analytical techniques, particularly diagnostic techniques. Conveniently the probes are provided in kit form. Different sets of probes may be used in techniques to prepare gene expression patterns and identify, diagnose or monitor different states, such as diseases, conditions or stages thereof. Also provided are methods of identifying suitable probes and their use in methods of the invention.

The identification of quick and easy methods of sample analysis for, for example, diagnostic applications, remains the goal of many researchers. End users seek methods which are cost effective, produce statistically significant results and which may be implemented routinely without the need for highly skilled individuals.

The analysis of gene expression within cells has been used to provide information on the state of those cells and importantly the state of the individual from which the cells are derived. The relative expression of various genes in a cell has been identified as reflecting a particular state within a body. For example, cancer cells are known to exhibit altered expression of various proteins and the transcripts or the expressed proteins may therefore be used as markers of that disease state.

Thus biopsy tissue may be analysed for the presence of these markers and cells originating from the site of the disease may be identified in other tissues or fluids of the body by the presence of the markers. Furthermore, products of the altered expression may be

released into the blood stream and these products may be analysed. In addition cells which have contacted disease cells may be affected by their direct contact with those cells resulting in altered gene expression and their expression or products of expression may be similarly analysed.

However, there are some limitations with these methods. For example, the use of specific tumour markers for identifying cancer suffers from a variety of defects, such as lack of specificity or sensitivity, association of the marker with disease states besides the specific type of cancer, and difficulty of detection in asymptomatic individuals.

In addition to the analysis of one or two marker transcripts or proteins, more recently, gene expression patterns have been analysed. Most of the work involving large-scale gene expression analysis with implications in disease diagnosis has involved clinical samples originating from diseased tissues or cells. For example, several recent publications, which demonstrate that gene expression data can be used to distinguish between similar cancer types, have used clinical samples from diseased tissues or cells (Alon et al. 1999, PNAS, 96, p6745-6750; Golub et al. 1999, Science, 286, p531-537; Alizadeh et al, 2000, Nature, 403, p503-511; Bittner et al., 2000, Nature, 406, p536-540).

However, these methods have relied on analysis of a sample containing diseased cells or products of those cells or cells which have been contacted by disease cells. Analysis of such samples relies on knowledge of the presence of a disease and its location, which may be difficult in asymptomatic patients. Furthermore, samples can not always be taken from the disease site, e.g. in diseases of the brain.

In a finding of great significance, the present inventors identified the previously untapped potential of all cells within a body to provide information

relating to the state of the organism from which the cells were derived. WO98/49342 describes the analysis of the gene expression of cells distant from the site of disease, e.g. peripheral blood collected distant from a cancer site.

This finding is based on the premise that the different parts of an organism's body exist in dynamic interaction with each other. When a disease affects one part of the body, other parts of the body are also affected. The interaction results from a wide spectrum of biochemical signals that are released from the diseased area, affecting other areas in the body. Although, the nature of the biochemical and physiological changes induced by the released signals can vary in the different body parts, the changes can be measured at the level of gene expression and used for diagnostic purposes.

The physiological state of a cell in an organism is determined by the pattern with which genes are expressed in it. The pattern depends upon the internal and external biological stimuli to which said cell is exposed, and any change either in the extent or in the nature of these stimuli can lead to a change in the pattern with which the different genes are expressed in the cell. There is a growing understanding that by analysing the systemic changes in gene expression patterns in cells in biological samples, it is possible to provide information on the type and nature of the biological stimuli that are acting on them. Thus, for example, by monitoring the expression of a large number of genes in cells in a test sample, it is possible to determine whether their genes are expressed with a pattern characteristic for a particular disease, condition or stage thereof. Measuring changes in gene activities in cells, e.g. from tissue or body fluids is therefore emerging as a powerful tool for disease diagnosis.

Such methods have various advantages. Often, obtaining clinical samples from certain areas in the body that is diseased can be difficult and may involve undesirable invasions in the body, for example biopsy is often used to obtain samples for cancer. In some cases, such as in Alzheimer's disease the diseased brain specimen can only be obtained post-mortem. Furthermore, the tissue specimens which are obtained are often heterogeneous and may contain a mixture of both diseased and non-diseased cells, making the analysis of generated gene expression data both complex and difficult.

It has been suggested that a pool of tumour tissues that appear to be pathogenetically homogeneous with respect to morphological appearances of the tumour may well be highly heterogeneous at the molecular level (Alizadeh, 2000, supra), and in fact might contain tumours representing essentially different diseases (Alizadeh, 2000, supra; Golub, 1999, supra). For the purpose of identifying a disease, condition, or a stage thereof, any method that does not require clinical samples to originate directly from diseased tissues or cells is highly desirable since clinical samples representing a homogeneous mixture of cell types can be obtained from an easily accessible region in the body.

We have now identified a set of probes of surprising utility for identifying one or more diseases. Thus, we now describe probes and sets of probes derived from cells which are not disease cells and which have not contacted disease cells, which correspond to genes which exhibit altered expression in normal versus disease individuals, for use in methods of identifying, diagnosing or monitoring certain conditions, particularly diseases or stages thereof.

Thus the invention provides a set of oligonucleotide probes which correspond to genes in a cell whose expression is affected in a pattern characteristic of a particular disease, condition or

stage thereof, wherein said genes are systemically affected by said disease, condition or stage thereof. Preferably said genes are metabolic or house-keeping genes and preferably are constitutively moderately or highly expressed. Preferably the genes are moderately or highly expressed in the cells of the sample but not in cells from disease cells or in cells having contacted such disease cells.

Such probes, particularly when isolated from cells distant to the site of disease, do not rely on the development of disease to clinically recognizable levels and allow detection of a disease or condition or stage thereof very early after the onset of said disease or condition, even years before other subjective or objective symptoms appear.

As used herein "systemically" affected genes refers to genes whose expression is affected in the body without direct contact with a disease cell or disease site and the cells under investigation are not disease cells.

"Contact" as referred to herein refers to cells coming into close proximity with one another such that the direct effect of one cell on the other may be observed, e.g. an immune response, wherein these responses are not mediated by secondary molecules released from the first cell over a large distance to affect the second cell. Preferably contact refers to physical contact, or contact that is as close as is sterically possible, conveniently, cells which contact one another are found in the same unit volume, for example within $1cm^3$.

A "disease cell" is a cell manifesting phenotypic changes and is present at the disease site at some time during its life-span, e.g. a tumour cell at the tumour site or which has disseminated from the tumour, or a brain cell in the case of brain disorders such as Alzheimer's disease.

"Metabolic" or "house-keeping" genes refer to those genes responsible for expressing products involved in cell division and maintenance, e.g. non-immune function related genes.

"Moderately or highly" expressed genes refers to those present in resting cells in a copy number of more than 30-100 copies/cell (assuming an average $3x10^5$ mRNA molecules in a cell).

Specific probes having the above described properties are provided herein.

Thus in one aspect, the present invention provides a set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from:

an oligonucleotide as described in Table 1 or derived from a sequence described in Table 1, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

"Table 1" as referred to herein refers to Table 1a and/or Table 1b. Table 1b contains reference to additional clones and sequences as disclosed herein. Similarly Tables 2 and 4 comprise 2 parts, a and b.

The invention also provides one or more oligonucleotide probes, wherein each oligonucleotide probe is selected from the oligonucleotides listed in Table 1, or derived from a sequence described in Table 1, or a complementary sequence thereof. The use of such probes in products and methods of the invention, form further aspects of the invention.

As referred to herein an "oligonucleotide" is a nucleic acid molecule having at least 6 monomers in the polymeric structure, ie. nucleotides or modified forms thereof. The nucleic acid molecule may be DNA, RNA or PNA (peptide nucleic acid) or hybrids thereof or modified versions thereof, e.g. chemically modified forms, e.g. LNA (Locked Nucleic acid), by methylation or made up of modified or non-natural bases during synthesis, providing they retain their ability to bind

to complementary sequences. Such oligonucleotides are used in accordance with the invention to probe target sequences and are thus referred to herein also as oligonucleotide probes or simply as probes.

An "oligonucleotide derived from a sequence described in Table 1" (or any other table) refers to a part of a sequence disclosed in that Table (e.g. Table 1-4), which satisfies the requirements of the oligonucleotide probes as described herein, e.g. in length and function. Preferably said parts have the size described hereinafter.

Preferably the oligonucleotide probes forming said set are at least 15 bases in length to allow binding of target molecules. Especially preferably said oligonucleotide probes are from 20 to 200 bases in length, e.g. from 30 to 150 bases, preferably 50-100 bases in length.

As referred to herein the term "complementary sequences" refers to sequences with consecutive complementary bases (ie. T:A, G:C) and which complementary sequences are therefore able to bind to one another through their complementarity.

Reference to "10 oligonucleotides" refers to 10 different oligonucleotides. Whilst a Table 1 oligonucleotide, a Table 1 derived oligonucleotide and their functional equivalent are considered different oligonucleotides, complementary oligonucleotides are not considered different. Preferably however, the at least 10 oligonucleotides are 10 different Table 1 oligonucleotides (or Table 1 derived oligonucleotides or their functional equivalents). Thus said 10 different oligonucleotides are preferably able to bind to 10 different transcripts.

Preferably said oligonucleotides are as described in Table 1 or are derived from a sequence described in Table 1. Especially preferably said oligonucleotides are as described in Table 2 or Table 4 or are derived

from a sequence described in either of those tables. Especially preferably the oligonucleotide (or the oligonucleotide derived therefrom) has a high occurrence as defined in Table 3, especially preferably >40%, e.g. >80 or >90, e.g. 100%.

A "set" as described refers to a collection of unique oligonucleotide probes (ie. having a distinct sequence) and preferably consists of less than 1000 oligonucleotide probes, especially less than 500 probes, e.g. preferably from 10 to 500, e.g. 10 to 100, 200 or 300, especially preferably 20 to 100, e.g. 30 to 100 probes. In some cases less than 10 probes may be used, e.g. from 2 to 9 probes, e.g. 5 to 9 probes.

It will be appreciated that increasing the number of probes will prevent the possibility of poor analysis, e.g. misdiagnosis by comparison to other diseases which could similarly alter the expression of the particular genes in question. Other oligonucleotide probes not described herein may also be present, particularly if they aid the ultimate use of the set of oligonucleotide probes. However, preferably said set consists only of said Table 1 oligonucleotides, Table 1 derived oligonucleotides, complementary sequences or functionally equivalent oligonucleotides, or a sub-set thereof (e.g. of the size as described above), preferably a sub-set for which sequences are provided herein (see Table 1 and its footnote). Especially preferably said set consists only of said Table 1 oligonucleotides, Table 1 derived oligonucleotides, or complementary sequences thereof, or a sub-set thereof.

Multiple copies of each unique oligonucleotide probe, e.g. 10 or more copies, may be present in each set, but constitute only a single probe.

A set of oligonucleotide probes, which may preferably be immobilized on a solid support or have means for such immobilization, comprises the at least 10 oligonucleotide probes selected from those described

hereinbefore. Especially preferably said probes are selected from those having high occurrence as described in Table 3 and as mentioned above. As mentioned above, these 10 probes must be unique and have different sequences. Having said this however, two separate probes may be used which recognize the same gene but reflect different splicing events. However oligonucleotide probes which are complementary to, and bind to distinct genes are preferred.

As described herein a "functionally equivalent" oligonucleotide to those described in Table 1 or derived therefrom refers to an oligonucleotide which is capable of identifying the same gene as an oligonucleotide of Table 1 or derived therefrom, ie. it can bind to the same mRNA molecule (or DNA) transcribed from a gene (target nucleic acid molecule) as the Table 1 oligonucleotide or the Table 1 derived oligonucleotide (or its complementary sequence). Preferably said functionally equivalent oligonucleotide is capable of recognizing, ie. binding to the same splicing product as a Table 1 oligonucleotide or a Table 1 derived oligonucleotide. Preferably said mRNA molecule is the full length mRNA molecule which corresponds to the Table 1 oligonucleotide or the Table 1 derived oligonucleotide.

As referred to herein "capable of binding" or "binding" refers to the ability to hybridize under conditions described hereinafter.

Alternatively expressed, functionally equivalent oligonucleotides (or complementary sequences) have sequence identity or will hybridize, as described hereinafter, to a region of the target molecule to which molecule a Table 1 oligonucleotide or a Table 1 derived oligonucleotide or a complementary oligonucleotide binds. Preferably, functionally equivalent oligonucleotides (or their complementary sequences) hybridize to one of the mRNA sequences which corresponds

to a Table 1 oligonucleotide or a Table 1 derived oligonucleotide under the conditions described hereinafter or has sequence identity to a part of one of the mRNA sequences which corresponds to a Table 1 oligonucleotide or a Table 1 derived oligonucleotide. A "part" in this context refers to a stretch of at least 5, e.g. at least 10 or 20 bases, such as from 5 to 100, e.g. 10 to 50 or 15 to 30 bases.

In a particularly preferred aspect, the functionally equivalent oligonucleotide binds to all or a part of the region of a target nucleic acid molecule (mRNA or cDNA) to which the Table 1 oligonucleotide or Table 1 derived oligonucleotide binds. A "target" nucleic acid molecule is the gene transcript or related product e.g. mRNA, or cDNA, or amplified product thereof. Said "region" of said target molecule to which said Table 1 oligonucleotide or Table 1 derived oligonucleotide binds is the stretch over which complementarity exists. At its largest this region is the whole length of the Table 1 oligonucleotide or Table 1 derived oligonucleotide, but may be shorter if the entire Table 1 sequence or Table 1 derived oligonucleotide is not complementary to a region of the target sequence.

Preferably said part of said region of said target molecule is a stretch of at least 5, e.g. at least 10 or 20 bases, such as from 5 to 100, e.g. 10 to 50 or 15 to 30 bases. This may for example be achieved by said functionally equivalent oligonucleotide having several identical bases to the bases of the Table 1 oligonucleotide or the Table 1 derived oligonucleotide. These bases may be identical over consecutive stretches, e.g. in a part of the functionally equivalent oligonucleotide, or may be present non-consecutively, but provide sufficient complementarity to allow binding to the target sequence.

Thus in a preferred feature, said functionally

equivalent oligonucleotide hybridizes under conditions of high stringency to a Table 1 oligonucleotide or a Table 1 derived oligonucleotide or the complementary sequence thereof. Alternatively expressed, said functionally equivalent oligonucleotide exhibits high sequence identity to all or part of a Table 1 oligonucleotide. Preferably said functionally equivalent oligonucleotide has at least 70% sequence identity, preferably at least 80%, e.g. at least 90, 95, 98 or 99%, to all of a Table 1 oligonucleotide or a part thereof. As used in this context, a "part" refers to a stretch of at least 5, e.g. at least 10 or 20 bases, such as from 5 to 100, e.g. 10 to 50 or 15 to 30 bases, in said Table 1 oligonucleotide. Especially preferably when sequence identity to only a part of said Table 1 oligonucleotide is present, the sequence identity is high, e.g. at least 80% as described above.

Functionally equivalent oligonucleotides which satisfy the above stated functional requirements include those which are derived from the Table 1 oligonucleotides and also those which have been modified by single or multiple nucleotide base (or equivalent) substitution, addition and/or deletion, but which nonetheless retain functional activity, e.g. bind to the same target molecule as the Table 1 oligonucleotide or the Table 1 derived oligonucleotide from which they are further derived or modified. Preferably said modification is of from 1 to 50, e.g. from 10 to 30, preferably from 1 to 5 bases. Especially preferably only minor modifications are present, e.g. variations in less than 10 bases, e.g. less than 5 base changes.

Within the meaning of "addition" equivalents are included oligonucleotides containing additional sequences which are complementary to the consecutive stretch of bases on the target molecule to which the Table 1 oligonucleotide or the Table 1 derived oligonucleotide binds. Alternatively the addition may

comprise a different, unrelated sequence, which may for example confer a further property, e.g. to provide a means for immobilization such as a linker to bind the oligonucleotide probe to a solid support.

Particularly preferred are naturally occurring equivalents such as biological variants, e.g. allelic, geographical or allotypic variants, e.g. oligonucleotides which correspond to a genetic variant, for example as present in a different species.

Functional equivalents include oligonucleotides with modified bases, e.g. using non-naturally occurring bases. Such derivatives may be prepared during synthesis or by post production modification.

"Hybridizing" sequences which bind under conditions of low stringency are those which bind under non-stringent conditions (for example, 6x SSC/50% formamide at room temperature) and remain bound when washed under conditions of low stringency (2 X SSC, room temperature, more preferably 2 X SSC, 42°C). Hybridizing under high stringency refers to the above conditions in which washing is performed at 2 X SSC, 65°C (where SSC = 0.15M NaCl, 0.015M sodium citrate, pH 7.2).

"Sequence identity" as referred to herein refers to the value obtained when assessed using ClustalW (Thompson et al., 1994, Nucl. Acids Res., 22, p4673-4680) with the following parameters:
Pairwise alignment parameters - Method: accurate, Matrix: IUB, Gap open penalty: 15.00, Gap extension penalty: 6.66;
Multiple alignment parameters - Matrix: IUB, Gap open penalty: 15.00, % identity for delay: 30, Negative matrix: no, Gap extension penalty: 6.66, DNA transitions weighting: 0.5.

Sequence identity at a particular base is intended to include identical bases which have simply been derivatized.

The invention also extends to polypeptides encoded

by the mRNA sequence to which a Table 1 oligonucleotide or a Table 1 derived oligonucleotide binds. The invention further extends to antibodies which bind to any of said polypeptides.

As described above, conveniently said set of oligonucleotide probes may be immobilized on one or more solid supports. Single or preferably multiple copies of each unique probe are attached to said solid supports, e.g. 10 or more, e.g. at least 100 copies of each unique probe are present.

One or more unique oligonucleotide probes may be associated with separate solid supports which together form a set of probes immobilized on multiple solid support, e.g. one or more unique probes may be immobilized on multiple beads, membranes, filters, biochips etc. which together form a set of probes, which together form modules of the kit described hereinafter. The solid support of the different modules are conveniently physically associated although the signals associated with each probe (generated as described hereinafter) must be separately determinable.

Alternatively, the probes may be immobilized on discrete portions of the same solid support, e.g. each unique oligonucleotide probe, e.g. in multiple copies, may be immobilized to a distinct and discrete portion or region of a single filter or membrane, e.g. to generate an array.

A combination of such techniques may also be used, e.g. several solid supports may be used which each immobilize several unique probes.

The expression "solid support" shall mean any solid material able to bind oligonucleotides by hydrophobic, ionic or covalent bridges.

"Immobilization" as used herein refers to reversible or irreversible association of the probes to said solid support by virtue of such binding. If reversible, the probes remain associated with the solid

support for a time sufficient for methods of the invention to be carried out.

Numerous solid supports suitable as immobilizing moieties according to the invention, are well known in the art and widely described in the literature and generally speaking, the solid support may be any of the well-known supports or matrices which are currently widely used or proposed for immobilization, separation etc. in chemical or biochemical procedures. Such materials include, but are not limited to, any synthetic organic polymer such as polystyrene, polyvinylchloride, polyethylene; or nitrocellulose and cellulose acetate; or tosyl activated surfaces; or glass or nylon or any surface carrying a group suited for covalent coupling of nucleic acids. The immobilizing moieties may take the form of particles, sheets, gels, filters, membranes, microfibre strips, tubes or plates, fibres or capillaries, made for example of a polymeric material e.g. agarose, cellulose, alginate, teflon, latex or polystyrene or magnetic beads. Solid supports allowing the presentation of an array, preferably in a single dimension are preferred, e.g. sheets, filters, membranes, plates or biochips.

Attachment of the nucleic acid molecules to the solid support may be performed directly or indirectly. For example if a filter is used, attachment may be performed by UV-induced crosslinking. Alternatively, attachment may be performed indirectly by the use of an attachment moiety carried on the oligonucleotide probes and/or solid support. Thus for example, a pair of affinity binding partners may be used, such as avidin, streptavidin or biotin, DNA or DNA binding protein (e.g. either the lac I repressor protein or the lac operator sequence to which it binds), antibodies (which may be mono- or polyclonal), antibody fragments or the epitopes or haptens of antibodies. In these cases, one partner of the binding pair is attached to (or is inherently

part of) the solid support and the other partner is attached to (or is inherently part of) the nucleic acid molecules.

As used herein an "affinity binding pair" refers to two components which recognize and bind to one another specifically (ie. in preference to binding to other molecules). Such binding pairs when bound together form a complex.

Attachment of appropriate functional groups to the solid support may be performed by methods well known in the art, which include for example, attachment through hydroxyl, carboxyl, aldehyde or amino groups which may be provided by treating the solid support to provide suitable surface coatings. Solid supports presenting appropriate moieties for attachment of the binding partner may be produced by routine methods known in the art.

Attachment of appropriate functional groups to the oligonucleotide probes of the invention may be performed by ligation or introduced during synthesis or amplification, for example using primers carrying an appropriate moiety, such as biotin or a particular sequence for capture.

Conveniently, the set of probes described hereinbefore is provided in kit form.

Thus viewed from a further aspect the present invention provides a kit comprising a set of oligonucleotide probes as described hereinbefore immobilized on one or more solid supports.

Preferably, said probes are immobilized on a single solid support and each unique probe is attached to a different region of said solid support. However, when attached to multiple solid supports, said multiple solid supports form the modules which make up the kit. Especially preferably said solid support is a sheet, filter, membrane, plate or biochip.

Optionally the kit may also contain information

relating to the signals generated by normal or diseased samples (as discussed in more detail hereinafter in relation to the use of the kits), standardizing materials, e.g. mRNA or cDNA from normal and/or diseased samples for comparative purposes, labels for incorporation into cDNA, adapters for introducing nucleic acid sequences for amplification purposes, primers for amplification and/or appropriate enzymes, buffers and solutions. Optionally said kit may also contain a package insert describing how the method of the invention should be performed, optionally providing standard graphs, data or software for interpretation of results obtained when performing the invention.

The use of such kits to prepare a standard diagnostic gene transcript pattern as described hereinafter forms a further aspect of the invention.

The set of probes as described herein have various uses. Principally however they are used to assess the gene expression state of a test cell to provide information relating to the organism from which said cell is derived. Thus the probes are useful in diagnosing, identifying or monitoring a disease or condition or stage thereof in an organism.

Thus in a further aspect the invention provides the use of a set of oligonucleotide probes or a kit as described hereinbefore to determine the gene expression pattern of a cell which pattern reflects the level of gene expression of genes to which said oligonucleotide probes bind, comprising at least the steps of:

a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotide probes or a kit as defined herein; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

The mRNA and cDNA as referred to in this method,

and the methods hereinafter, encompass derivatives or copies of said molecules, e.g. copies of such molecules such as those produced by amplification or the preparation of complementary strands, but which retain the identity of the mRNA sequence, ie. would hybridize to the direct transcript (or its complementary sequence) by virtue of precise complementarity, or sequence identity, over at least a region of said molecule. It will be appreciated that complementarity will not exist over the entire region where techniques have been used which may truncate the transcript or introduce new sequences, e.g. by primer amplification. For convenience, said mRNA or cDNA is preferably amplified prior to step b). As with the oligonucleotides described herein said molecules may be modified, e.g. by using non-natural bases during synthesis providing complementarity remains. Such molecules may also carry additional moieties such as signalling or immobilizing means.

The various steps involved in the method of preparing such a pattern are described in more detail hereinafter.

As used herein "gene expression" refers to transcription of a particular gene to produce a specific mRNA product (ie. a particular splicing product). The level of gene expression may be determined by assessing the level of transcribed mRNA molecules or cDNA molecules reverse transcribed from the mRNA molecules or products derived from those molecules, e.g. by amplification.

The "pattern" created by this technique refers to information which, for example, may be represented in tabular or graphical form and conveys information about the signal associated with two or more oligonucleotides. Preferably said pattern is expressed as an array of numbers relating to the expression level associated with each probe.

Preferably, said pattern is established using the following linear model:

$$y = \mathbf{Xb} + \mathbf{f} \qquad \text{Equation 1}$$

wherein, **X** is the matrix of gene expression data and **y** is the response variable, **b** is the regression coefficient vector and **f** the estimated residual vector. Although many different methods can be used to establish the relationship provided in equation 1, especially preferably the partial Least Squares Regression (PLSR) method is used for establishing the relationship in equation 1.

The probes are thus used to generate a pattern which reflects the gene expression of a cell at the time of its isolation. The pattern of expression is characteristic of the circumstances under which that cells finds itself and depends on the influences to which the cell has been exposed. Thus, a characteristic gene transcript pattern standard or fingerprint (standard probe pattern) for cells from an individual with a particular disease or condition may be prepared and used for comparison to transcript patterns of test cells. This has clear applications in diagnosing, monitoring or identifying whether an organism is suffering from a particular disease, condition or stage thereof.

The standard pattern is prepared by determining the extent of binding of total mRNA (or cDNA or related product), from cells from a sample of one or more organisms with the disease or condition or stage thereof, to the probes. This reflects the level of transcripts which are present which correspond to each unique probe. The amount of nucleic acid material which binds to the different probes is assessed and this information together forms the gene transcript pattern standard of that disease or condition or stage thereof. Each such standard pattern is characteristic of the disease, condition or stage thereof.

In a further aspect therefore, the present invention provides a method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as described hereinbefore specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in the sample with the disease, condition or stage thereof.

For convenience, said oligonucleotides are preferably immobilized on one or more solid supports.

The standard pattern for a great number of diseases or conditions and different stages thereof using particular probes may be accumulated in databases and be made available to laboratories on request.

"Disease" samples and organisms as referred to herein refer to organisms (or samples from the same) with an underlying pathological disturbance relative to a normal organism (or sample), in a symptomatic or asymptomatic organism, which may result, for example, from infection or an acquired or congenital genetic imperfection. Such organisms are known to have, or which exhibit, the disease or condition or stage thereof under study.

A "condition" refers to a state of the mind or body of an organism which has not occurred through disease,

e.g. the presence of an agent in the body such as a toxin, drug or pollutant, or pregnancy.

"Stages" thereof refer to different stages of the disease or condition which may or may not exhibit particular physiological or metabolic changes, but do exhibit changes at the genetic level which may be detected as altered gene expression. It will be appreciated that during the course of a disease or condition the expression of different transcripts may vary. Thus at different stages, altered expression may not be exhibited for particular transcripts compared to "normal" samples. However, combining information from several transcripts which exhibit altered expression at one or more stages through the course of the disease or condition can be used to provide a characteristic pattern which is indicative of a particular stage of the disease or condition. Thus for example different stages in cancer, e.g. pre-stage I, stage I, stage II, II or IV can be identified.

"Normal" as used herein refers to organisms or samples which are used for comparative purposes. Preferably, these are "normal" in the sense that they do not exhibit any indication of, or are not believed to have, any disease or condition that would affect gene expression, particularly in respect of the disease for which they are to be used as the normal standard. However, it will be appreciated that different stages of a disease or condition may be compared and in such cases, the "normal" sample may correspond to the earlier stage of the disease or condition.

As used herein a "sample" refers to any material obtained from the organism, e.g. human or non-human animal under investigation which contains cells and includes, tissues, body fluid or body waste or in the case of prokaryotic organisms, the organism itself. "Body fluids" include blood, saliva, spinal fluid, semen, lymph. "Body waste" includes urine, expectorated

matter (pulmonary patients), faeces etc. "Tissue samples" include tissue obtained by biopsy, by surgical interventions or by other means e.g. placenta. Preferably however, the samples which are examined are from areas of the body not apparently affected by the disease or condition. The cells in such samples are not disease cells, e.g. cancer cells, have not been in contact with such disease cells and do not originate from the site of the disease or condition. The "site of disease" is considered to be that area of the body which manifests the disease in a way which may be objectively determined, e.g. a tumour or area of inflammation. Thus for example peripheral blood may be used for the diagnosis of non-haematopoietic cancers, and the blood does not require the presence of malignant or disseminated cells from the cancer in the blood. Similarly in diseases of the brain, in which no diseased cells are found in the blood due to the blood:brain barrier, peripheral blood may still be used in the methods of the invention.

It will however be appreciated that the method of preparing the standard transcription pattern and other methods of the invention are also applicable for use on living parts of eukaryotic organisms such as cell lines and organ cultures and explants.

As used herein, reference to "corresponding" sample etc. refers to cells preferably from the same tissue, body fluid or body waste, but also includes cells from tissue, body fluid or body waste which are sufficiently similar for the purposes of preparing the standard or test pattern. When used in reference to genes "corresponding" to the probes, this refers to genes which are related by sequence (which may be complementary) to the probes although the probes may reflect different splicing products of expression.

"Assessing" as used herein refers to both quantitative and qualitative assessment which may be

determined in absolute or relative terms.

The invention may be put into practice as follows. To prepare a standard transcript pattern for a particular disease, condition or stage thereof, sample mRNA is extracted from the cells of tissues, body fluid or body waste according to known techniques (see for example Sambrook et. al. (1989), Molecular Cloning : A laboratory manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.) from a diseased individual or organism.

Owing to the difficulties in working with RNA, the RNA is preferably reverse transcribed at this stage to form first strand cDNA. Cloning of the cDNA or selection from, or using, a cDNA library is not however necessary in this or other methods of the invention. Preferably, the complementary strands of the first strand cDNAs are synthesized, ie. second strand cDNAs, but this will depend on which relative strands are present in the oligonucleotide probes. The RNA may however alternatively be used directly without reverse transcription and may be labelled if so required.

Preferably the cDNA strands are amplified by known amplification techniques such as the polymerase chain reaction (PCR) by the use of appropriate primers. Alternatively, the cDNA strands may be cloned with a vector, used to transform a bacteria such as E. coli which may then be grown to multiply the nucleic acid molecules. When the sequence of the cDNAs are not known, primers may be directed to regions of the nucleic acid molecules which have been introduced. Thus for example, adapters may be ligated to the cDNA molecules and primers directed to these portions for amplification of the cDNA molecules. Alternatively, in the case of eukaryotic samples, advantage may be taken of the polyA tail and cap of the RNA to prepare appropriate primers.

To produce the standard diagnostic gene transcript pattern or fingerprint for a particular disease or

condition or stage thereof, the above described oligonucleotide probes are used to probe mRNA or cDNA of the diseased sample to produce a signal for hybridization to each particular oligonucleotide probe species, ie. each unique probe. A standard control gene transcript pattern may also be prepared if desired using mRNA or cDNA from a normal sample. Thus, mRNA or cDNA is brought into contact with the oligonucleotide probe under appropriate conditions to allow hybridization.

When multiple samples are probed, this may be performed consecutively using the same probes, e.g. on one or more solid supports, ie. on probe kit modules, or by simultaneously hybridizing to corresponding probes, e.g. the modules of a corresponding probe kit.

To identify when hybridization occurs and obtain an indication of the number of transcripts/cDNA molecules which become bound to the oligonucleotide probes, it is necessary to identify a signal produced when the transcripts (or related molecules) hybridize (e.g. by detection of double stranded nucleic acid molecules or detection of the number of molecules which become bound, after removing unbound molecules, e.g. by washing).

In order to achieve a signal, either or both components which hybridize (ie. the probe and the transcript) carry or form a signalling means or a part thereof. This "signalling means" is any moiety capable of direct or indirect detection by the generation or presence of a signal. The signal may be any detectable physical characteristic such as conferred by radiation emission, scattering or absorption properties, magnetic properties, or other physical properties such as charge, size or binding properties of existing molecules (e.g. labels) or molecules which may be generated (e.g. gas emission etc.). Techniques are preferred which allow signal amplification, e.g. which produce multiple signal events from a single active binding site, e.g. by the catalytic action of enzymes to produce multiple

detectable products.

Conveniently the signalling means may be a label which itself provides a detectable signal. Conveniently this may be achieved by the use of a radioactive or other label which may be incorporated during cDNA production, the preparation of complementary cDNA strands, during amplification of the target mRNA/cDNA or added directly to target nucleic acid molecules.

Appropriate labels are those which directly or indirectly allow detection or measurement of the presence of the transcripts/cDNA. Such labels include for example radiolabels, chemical labels, for example chromophores or fluorophores (e.g. dyes such as fluorescein and rhodamine), or reagents of high electron density such as ferritin, haemocyanin or colloidal gold. Alternatively, the label may be an enzyme, for example peroxidase or alkaline phosphatase, wherein the presence of the enzyme is visualized by its interaction with a suitable entity, for example a substrate. The label may also form part of a signalling pair wherein the other member of the pair is found on, or in close proximity to, the oligonucleotide probe to which the transcript/cDNA binds, for example, a fluorescent compound and a quench fluorescent substrate may be used. A label may also be provided on a different entity, such as an antibody, which recognizes a peptide moiety attached to the transcripts/cDNA, for example attached to a base used during synthesis or amplification.

A signal may be achieved by the introduction of a label before, during or after the hybridization step. Alternatively, the presence of hybridizing transcripts may be identified by other physical properties, such as their absorbance, and in which case the signalling means is the complex itself.

The amount of signal associated with each oligonucleotide probe is then assessed. The assessment may be quantitative or qualitative and may be based on

binding of a single transcript species (or related cDNA or other products) to each probe, or binding of multiple transcript species to multiple copies of each unique probe. It will be appreciated that quantitative results will provide further information for the transcript fingerprint of the disease which is compiled. This data may be expressed as absolute values (in the case of macroarrays) or may be determined relative to a particular standard or reference e.g. a normal control sample.

Furthermore it will be appreciated that the standard diagnostic gene pattern transcript may be prepared using one or more disease samples (and normal samples if used) to perform the hybridization step to obtain patterns not biased towards a particular individual's variations in gene expression.

The use of the probes to prepare standard patterns and the standard diagnostic gene transcript patterns thus produced for the purpose of identification or diagnosis or monitoring of a particular disease or condition or stage thereof in a particular organism forms a further aspect of the invention.

Once a standard diagnostic fingerprint or pattern has been determined for a particular disease or condition using the selected oligonucleotide probes, this information can be used to identify the presence, absence or extent or stage of that disease or condition in a different test organism or individual.

To examine the gene expression pattern of a test sample, a test sample of tissue, body fluid or body waste containing cells, corresponding to the sample used for the preparation of the standard pattern, is obtained from a patient or the organism to be studied. A test gene transcript pattern is then prepared as described hereinbefore as for the standard pattern.

In a further aspect therefore, the present invention provides a method of preparing a test gene

transcript pattern comprising at least the steps of:

a) isolating mRNA from the cells of a sample of said test organism, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as described hereinbefore specific for a disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in said test sample.

This test pattern may then be compared to one or more standard patterns to assess whether the sample contains cells having the disease, condition or stage thereof.

Thus viewed from a further aspect the present invention provides a method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

a) isolating mRNA from the cells of a sample of said organism, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as described hereinbefore specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation;

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in said sample; and

d) comparing said pattern to a standard

diagnostic pattern prepared according to the method of the invention using a sample from an organism corresponding to the organism and sample under investigation to determine the presence of said disease or condition or a stage thereof in the organism under investigation.

The method up to and including step c) is the preparation of a test pattern as described above.

As referred to herein, "diagnosis" refers to determination of the presence or existence of a disease or condition or stage thereof in an organism. "Monitoring" refers to establishing the extent of a disease or condition, particularly when an individual is known to be suffering from a disease or condition, for example to monitor the effects of treatment or the development of a disease or condition, e.g. to determine the suitability of a treatment or provide a prognosis.

The presence of the disease or condition or stage thereof may be determined by determining the degree of correlation between the standard and test samples' patterns. This necessarily takes into account the range of values which are obtained for normal and diseased samples. Although this can be established by obtaining standard deviations for several representative samples binding to the probes to develop the standard, it will be appreciated that single samples may be sufficient to generate the standard pattern to identify a disease if the test sample exhibits close enough correlation to that standard. Conveniently, the presence, absence, or extent of a disease or condition or stage thereof in a test sample can be predicted by inserting the data relating to the expression level of informative probes in test sample into the standard diagnostic probe pattern established according to equation 1.

Data generated using the above mentioned methods may be analysed using various techniques from the most

basic visual representation (e.g. relating to intensity) to more complex data manipulation to identify underlying patterns which reflect the interrelationship of the level of expression of each gene to which the various probes bind, which may be quantified and expressed mathematically. Conveniently, the raw data thus generated may be manipulated by the data processing and statistical methods described hereinafter, particularly normalizing and standardizing the data and fitting the data to a classification model to determine whether said test data reflects the pattern of a particular disease, condition or stage thereof.

The methods described herein may be used to identify, monitor or diagnose a disease, condition or ailment or its stage or progression, for which the oligonucleotide probes are informative. "Informative" probes as described herein, are those which reflect genes which have altered expression in the diseases or conditions in question, or particular stages thereof. Probes of the invention may not be sufficiently informative for diagnostic purposes when used alone, but are informative when used as one of several probes to provide a characteristic pattern, e.g. in a set as described hereinbefore.

Preferably said probes correspond to genes which are systemically affected by said disease, condition or stage thereof. Especially preferably said genes, from which transcripts are derived which bind to probes of the invention, are metabolic or house-keeping genes and preferably are moderately or highly expressed. The advantage of using probes directed to moderately or highly expressed genes is that smaller clinical samples are required for generating the necessary gene expression data set, e.g. less than 1ml blood samples.

Furthermore, it has been found that such genes which are already being actively transcribed tend to be more prone to being influenced, in a positive or

negative way, by new stimuli. In addition, since transcripts are already being produced at levels which are generally detectable, small changes in those levels are readily detectable as for example, a certain detectable threshold does not need to be reached.

In preferred methods of the invention, the set of probes of the invention are informative for a variety of different diseases, conditions or stages thereof. A sub-set of the probes disclosed herein may be used for diagnosis, identification or monitoring a particular disease, condition or stage thereof.

Thus the probes may be used to diagnose or identify or monitor any condition, ailment, disease or reaction that leads to the relative increase or decrease in the activity of informative genes of any or all eukaryotic or prokaryotic organisms regardless of whether these changes have been caused by the influence of bacteria, virus, prions, parasites, fungi, radiation, natural or artificial toxins, drugs or allergens, including mental conditions due to stress, neurosis, psychosis or deteriorations due to the ageing of the organism, and conditions or diseases of unknown cause, providing a sub-set of the probes as described herein are informative for said disease or condition or stage thereof.

Such diseases include those which result in metabolic or physiological changes, such as fever-associated diseases such as influenza or malaria. Other diseases which may be detected include for example yellow fever, sexually transmitted diseases such as gonorrhea, fibromyalgia, candida-related complex, cancer (for example of the stomach, lung, breast, prostate gland, bowel, skin, colon, ovary etc), Alzheimer's disease, disease caused by retroviruses such as HIV, senile dementia, multiple sclerosis and Creutzfeldt-Jakob disease to mention a few.

The invention may also be used to identify patients

with psychiatric or psychosomatic diseases such as schizophrenia and eating disorders. Of particular importance is the use of this method to detect diseases, conditions, or stages thereof, which are not readily detectable by known diagnostic methods, such as HIV which is generally not detectable using known techniques 1 to 4 months following infection. Conditions which may be identified include for example drug abuse, such as the use of narcotics, alcohol, steroids or performance enhancing drugs.

Preferably said disease to be identified or monitored is a cancer or a degenerative brain disorder (such as Alzheimer's or Parkinson's disease).

In particular, a set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from:

an oligonucleotide as described in Table 4 or an oligonucleotide derived therefrom or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide,

may be used for diagnosis or identification or monitoring the progression of Alzheimer's disease. Similarly Table 2 probes and Table 2 derived probes and their functional equivalents may be used to diagnose, identify or monitor the progression of breast cancer. Especially preferably the probes used for breast cancer analysis are selected based on their occurrence as set forth in Table 3 and as described hereinbefore.

The diagnostic method may be used alone as an alternative to other diagnostic techniques or in addition to such techniques. For example, methods of the invention may be used as an alternative or additive diagnostic measure to diagnosis using imaging techniques such as Magnetic Resonance Imagine (MRI), ultrasound imaging, nuclear imaging or X-ray imaging, for example in the identification and/or diagnosis of tumours.

The methods of the invention may be performed on

cells from prokaryotic or eukaryotic organisms which may be any eukaryotic organisms such as human beings, other mammals and animals, birds, insects, fish and plants, and any prokaryotic organism such as a bacteria.

Preferred non-human animals on which the methods of the invention may be conducted include, but are not limited to mammals, particularly primates, domestic animals, livestock and laboratory animals. Thus preferred animals for diagnosis include mice, rats, guinea pigs, cats, dogs, pigs, cows, goats, sheep, horses. Particularly preferably the disease state or condition of humans is diagnosed, identified or monitored.

As described above, the sample under study may be any convenient sample which may be obtained from an organism. Preferably however, as mentioned above, the sample is obtained from a site distant to the site of disease and the cells in such samples are not disease cells, have not been in contact with such cells and do not originate from the site of the disease or condition. In such cases, although preferably absent, the sample may contain cells which do not fulfil these criteria. However, since the probes of the invention are concerned with transcripts whose expression is altered in cells which do satisfy these criteria, the probes are specifically directed to detecting changes in transcript levels in those cells even if in the presence of other, background cells.

It has been found that the cells from such samples show significant and informative variations in the gene expression of a large number of genes. Thus, the same probe (or several probes) may be found to be informative in determinations regarding two or more diseases, conditions or stages thereof by virtue of the particular level of transcripts binding to that probe or the interrelationship of the extent of binding to that probe relative to other probes. As a consequence, it is

possible to use a relatively small number of probes for screening for multiple disorders or diseases. This has consequences with regard to the selection of probes, discussed in relation to random identification of probes hereinafter, but also for the use of a single set of probes for more than one diagnosis. Table 9 which represents preferred probes of the invention discloses probes which are informative for both Alzheimer's and breast cancer.

Thus, the present invention also provides sets of probes for diagnosing, identifying or monitoring two or more diseases, conditions or stages thereof, wherein at least one of said probes is suitable for said diagnosing, identifying or monitoring at least two of said diseases, conditions or stages thereof, and kits and methods of using the same. Preferably at least 5 probes, e.g. from 5 to 15 probes, are used in at least two diagnoses.

Thus, in a further preferred aspect, the present invention provides a method of diagnosis or identification or monitoring as described hereinbefore for the diagnosis, identification or monitoring of two or more diseases, conditions or stages thereof in an organism, wherein said test pattern produced in step c) of the diagnostic method is compared in step d) to at least two standard diagnostic patterns prepared as described previously, wherein each standard diagnostic pattern is a pattern generated for a different disease or condition or stage thereof.

Whilst in a preferred aspect the methods of assessment concern the development of a gene transcript pattern from a test sample and comparison of the same to a standard pattern, the elevation or depression of expression of certain markers may also be examined by examining the products of expression and the level of those products. Thus a standard pattern in relation to the expressed product may be generated.

In such methods the levels of expression of a set of polypeptides encoded by the gene to which an oligonucleotide of Table 1 or a Table 1 derived oligonucleotide, binds, are analysed.

Various diagnostic methods may be used to assess the amount of polypeptides (or fragments thereof) which are present. The presence or concentration of polypeptides may be examined, for example by the use of a binding partner to said polypeptide (e.g. an antibody), which may be immobilized, to separate said polypeptide from the sample and the amount of polypeptide may then be determined.

"Fragments" of the polypeptides refers to a domain or region of said polypeptide, e.g. an antigenic fragment, which is recognizable as being derived from said polypeptide to allow binding of a specific binding partner. Preferably such a fragment comprises a significant portion of said polypeptide and corresponds to a product of normal post-synthesis processing.

Thus in a further aspect the present invention provides a method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) releasing target polypeptides from a sample of one or more organisms having the disease or condition or stage thereof;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides, in the sample with the disease, condition or stage thereof.

As used herein "target polypeptides" refer to those polypeptides present in a sample which are to be detected and "marker polypeptides" are polypeptides which are encoded by the genes to which Table 1 oligonucleotides or Table 1 derived oligonucleotides bind. The target and marker polypeptides are identical or at least have areas of high similarity, e.g. epitopic regions to allow recognition and binding of the binding partner.

"Release" of the target polypeptides refers to appropriate treatment of a sample to provide the polypeptides in a form accessible for binding of the binding partners, e.g. by lysis of cells where these are present. The samples used in this case need not necessarily comprise cells as the target polypeptides may be released from cells into the surrounding tissue or fluid, and this tissue or fluid may be analysed, e.g. urine or blood. Preferably however the preferred samples as described herein are used. "Binding partners" comprise the separate entities which together make an affinity binding pair as described above, wherein one partner of the binding pair is the target or marker polypeptide and the other partner binds specifically to that polypeptide, e.g. an antibody.

Various arrangements may be envisaged for detecting the amount of binding pairs which form. In its simplest form, a sandwich type assay e.g. an immunoassay such as an ELISA, may be used in which an antibody specific to the polypeptide and carrying a label (as described elsewhere herein) may be bound to the binding pair (e.g. the first antibody:polypeptide pair) and the amount of label detected.

Other methods as described herein may be similarly modified for analysis of the protein product of expression rather than the gene transcript and related nucleic acid molecules.

Thus a further aspect of the invention provides a method of preparing a test gene transcript pattern comprising at least the steps of:

a) releasing target polypeptides from a sample of said test organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides, in said test sample.

A yet further aspect of the invention provides a method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism comprising the steps of:

a) releasing target polypeptides from a sample of said organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an

organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides in said sample; and

d) comparing said pattern to a standard diagnostic pattern prepared as described hereinbefore using a sample from an organism corresponding to the organism and sample under investigation to determine the degree of correlation indicative of the presence of said disease or condition or a stage thereof in the organism under investigation.

The methods of generating standard and test patterns and diagnostic techniques rely on the use of informative oligonucleotide probes to generate the gene expression data. In some cases it will be necessary to select these informative probes for a particular method, e.g. to diagnose a particular disease, from a selection of available probes, e.g. the probes described hereinbefore (the Table 1 oligonucleotides, the Table 1 derived oligonucleotides, their complementary sequences and functionally equivalent oligonucleotides). The following methodology describes a convenient method for identifying such informative probes, or more particularly how to select a suitable sub-set of probes from the probes described herein.

Probes for the analysis of a particular disease or condition or stage thereof, may be identified in a number of ways known in the prior art, including by differential expression or by library subtraction (see for example WO98/49342). As described hereinafter, in view of the high information content of most transcripts, as a starting point one may also simply analyse a random sub-set of mRNA or cDNA species and pick the most informative probes from that sub-set. The following method describes the use of immobilized

oligonucleotide probes (e.g. the probes of the invention) to which mRNA (or related molecules) from different samples is bound to identify which probes are the most informative to identify a particular type of sample, e.g. a disease sample.

The immobilized probes can be derived from various unrelated or related organisms; the only requirement is that the immobilized probes should bind specifically to their homologous counterparts in test organisms. Probes can also be derived from commercially available or public databases and immobilized on solid supports or, as mentioned above, they can be randomly picked and isolated from a cDNA library and immobilized on a solid support.

The length of the probes immobilised on the solid support should be long enough to allow for specific binding to the target sequences. The immobilised probes can be in the form of DNA, RNA or their modified products or PNAs (peptide nucleic acids). Preferably, the probes immobilised should bind specifically to their homologous counterparts representing highly and moderately expressed genes in test organisms. Conveniently the probes which are used are the probes described herein.

The gene expression pattern of cells in biological samples can be generated using prior art techniques such as microarray or macroarray as described below or using methods described herein. Several technologies have now been developed for monitoring the expression level of a large number of genes simultaneously in biological samples, such as, high-density oligoarrays (Lockhart et al., 1996, Nat. Biotech., 14, p1675-1680), cDNA microarrays (Schena et al, 1995, Science, 270, p467-470) and cDNA macroarrays (Maier E et al., 1994, Nucl. Acids Res., 22, p3423-3424; Bernard et al., 1996, Nucl. Acids Res., 24, p1435-1442).

In high-density oligoarrays and cDNA microarrays,

hundreds and thousands of probe oligonucleotides or cDNAs, are spotted onto glass slides or nylon membranes, or synthesized on biochips. The mRNA isolated from the test and reference samples are labelled by reverse transcription with a red or green fluorescent dye, mixed, and hybridised to the microarray. After washing, the bound fluorescent dyes are detected by a laser, producing two images, one for each dye. The resulting ratio of the red and green spots on the two images provides the information about the changes in expression levels of genes in the test and reference samples. Alternatively, single channel or multiple channel microarray studies can also be performed.

In cDNA macroarray, different cDNAs are spotted on a solid support such as nylon membranes in excess in relation to the amount of test mRNA that can hybridise to each spot. mRNA isolated from test samples is radio-labelled by reverse transcription and hybridised to the immobilised probe cDNA. After washing, the signals associated with labels hybridising specifically to immobilised probe cDNA are detected and quantified. The data obtained in macroarray contains information about the relative levels of transcripts present in the test samples. Whilst macroarrays are only suitable to monitor the expression of a limited number of genes, microarrays can be used to monitor the expression of several thousand genes simultaneously and is, therefore, a preferred choice for large-scale gene expression studies.

A macroarray technique for generating the gene expression data set has been used to illustrate the probe identification method described herein. For this purpose, mRNA is isolated from samples of interest and used to prepare labelled target molecules, e.g. mRNA or cDNA as described above. The labelled target molecules are then hybridised to probes immobilised on the solid support. Various solid supports can be used for the

purpose, as described previously. Following hybridization, unbound target molecules are removed and signals from target molecules hybridizing to immobilised probes quantified. If radio labelling is performed, PhosphoImager can be used to generate an image file that can be used to generate a raw data set. Depending on the nature of label chosen for labelling the target molecules, other instruments can also be used, for example, when fluorescence is used for labelling, a FluoroImager can be used to generate an image file from the hybridised target molecules.

The raw data corresponding to mean intensity, median intensity, or volume of the signals in each spot can be acquired from the image file using commercially available software for image analysis. However, the acquired data needs to be corrected for background signals and normalized prior to analysis, since, several factors can affect the quality and quantity of the hybridising signals. For example, variations in the quality and quantity of mRNA isolated from sample to sample, subtle variations in the efficiency of labelling target molecules during each reaction, and variations in the amount of unspecific binding between different macroarrays can all contribute to noise in the acquired data set that must be corrected for prior to analysis.

Background correction can be performed in several ways. The lowest pixel intensity within a spot can be used for background subtraction or the mean or median of the line of pixels around the spots' outline can be used for the purpose. One can also define an area representing the background intensity based on the signals generated from negative controls and use the average intensity of this area for background subtraction.

The background corrected data can then be transformed for stabilizing the variance in the data structure and normalized for the differences in probe

intensity. Several transformation techniques have been described in the literature and a brief overview can be found in Cui, Kerr and Churchill http://www.jax.org/research/churchill/research/expression/Cui-Transform.pdf). Normalization can be performed by dividing the intensity of each spot with the collective intensity, average intensity or median intensity of all the spots in a macroarray or a group of spots in a macroarray in order to obtain the relative intensity of signals hybridising to immobilised probes in a macroarray. Several methods have been described for normalizing gene expression data (Richmond and Somerville, 2000, Current Opin. Plant Biol., 3, p108-116; Finkelstein et al., 2001, In "Methods of Microarray Data Analysis. Papers from CAMDA, Eds. Lin & Johnsom, Kluwer Academic, p57-68; Yang et al., 2001, In "Optical Technologies and Informatics", Eds. Bittner, Chen, Dorsel & Dougherty, Proceedings of SPIE, 4266, p141-152; Dudoit et al, 2000, J. Am. Stat. Ass., 97, p77-87; Alter et al 2000, supra; Newton et al., 2001, J. Comp. Biol., 8, p37-52). Generally, a scaling factor or function is first calculated to correct the intensity effect and then used for normalising the intensities. The use of external controls has also been suggested for improved normalization.

One other major challenge encountered in large-scale gene expression analysis is that of standardization of data collected from experiments performed at different times. We have observed that gene expression data for samples acquired in the same experiment can be efficiently compared following background correction and normalization. However, the data from samples acquired in experiments performed at different times requires further standardization prior to analysis. This is because subtle differences in experimental parameters between different experiments, for example, differences in the quality and quantity of

mRNA extracted at different times, differences in time used for target molecule labelling, hybridization time or exposure time, can affect the measured values. Also, factors such as the nature of the sequence of transcripts under investigation (their GC content) and their amount in relation to the each other determines how they are affected by subtle variations in the experimental processes. They determine, for example, how efficiently first strand cDNAs, corresponding to a particular transcript, are transcribed and labelled during first strand synthesis, or how efficiently the corresponding labelled target molecules bind to their complementary sequences during hybridization. Batch to batch difference in the printing process is also a major factor for variation in the generated expression data.

Failure to properly address and rectify for these influences leads to situations where the differences between the experimental series may overshadow the main information of interest contained in the gene expression data set, i.e. the differences within the combined data from the different experimental series. Figure 1 provides one such example showing a classification based on Principal Component Analysis (PCA) of combined data from two experimental series where the main goal is to distinguish between Alzheimer/non-Alzheimer patients.

PCA (also known as singular value decomposition) is a technique for studying interdependencies and underlying relationships of a set of variables. The data are modelled in terms of a few significant factors or principal components (PC's), plus residuals. The PC's contain the main phenomena and define the systematic variability present in the data, while the residuals represent the variability interpreted as noise. Details on PCA can be found in Jollife (1986, Principal Component Analysis, Springer-Verlag, NY), and Jackson (1991, A User's Guide to Principal Components, Wiley, NY). The results of Figure 1 show that two

clusters are formed representing the data from two experimental series rather than the Alzheimer/non-Alzheimer differentiation. There were eight samples in common between the two series of experiments, which ideally should have fallen on top of, or in near proximity to, each other if appropriately standardized.

We have now found that gene expression data between different experiments can be efficiently standardized by including a subset of samples from one experimental series in the next experimental series and using a direct standardization method (DS), originally described by Wang and Kowalski (Anal. Chem., 1991, 63, p2750 and J. Chemometrics, 1991, 5, p129-145). Although the method of DS is well known in the field of analytical chemistry, it remains undescribed and unused in the field of gene expression data analysis.

In DS, the secondary data representing for example experimental series 2 (secondary measurements, R_2) are corrected to match the data measured on the primary measurements representing data from series 1 (R_1), while the calibration model remains unchanged. In DS, response matrices for both experimental series are related to each other by a transformation matrix F, i.e.

$$R_1 = R_2F \qquad (1)$$

Where F is a square matrix dimensioned gene by gene. From (1), the transformation matrix is calculated as:

$$F = R_2^{+}R_1 \qquad (2)$$

The transformation matrix F in equation (2) is calculated using a relatively small subset of samples which are measured on both the master primary and the secondary series of data.

Finally, the response of the unknown sample measured on the secondary series $r^{T}_{2,un}$, is standardized

to the response vector $\hat{r}^T_{1,un}$ expected from the primary series

$$\hat{r}^T_{1,un} = rT_{21,un}\hat{F} \qquad (3)$$

From the preceding equation it can be seen that the column i of the transformation matrix contains the multiplication factors for a set of genes measured in the secondary series to obtain the intensity at spot i of the corrected series.

The number of samples that are repeated in the experimental series, R_1 and R_2, should be equal to their ranks, which in this case is equal to the number of principal components retained for explaining the variation in the R_1 and R_2. For example, if three principal components are retained for explaining the variation in the data set, a minimum of three samples should be repeated between R_1 and R_2. The samples that should be repeated between different series should ideally be those that exhibit high leverages in the gene expression pattern. At times, two samples may suffice, while at other times, more than two samples should be ideally be included for good representativity. In some cases, the samples selected can be the same in all the experimental series to be compared (reference samples), while in other cases, representative samples can be selected sequentially by analyzing the expression pattern after each experiment. The selected samples with high leverages are then included in the next experimental series. The results of using Direct Standardization are shown in Figure 1.

Another approach for normalizing and standardizing the gene expression data set is to hybridize each DNA array with target molecules prepared from a test sample and an equal amount of labelled target molecules prepared from representative reference samples. In order to measure the intensity of labelled target

molecules hybridizing to the immobilized probes it is necessary that the labelled molecules are prepared from test and reference samples using different labels, for example, different fluorescent dyes can be used for preparing the labelled material. The labelled molecules prepared from reference samples can be added to the hybridization solution together with the labelled material prepared from test samples. A data file from each array representing the expression pattern of different genes in the test sample and reference samples can then be obtained, normalized and standardized by the direct standardization method as described above. An instant advantage of including the differentially labelled target molecules from reference samples during hybridization is that it enables an efficient comparison of new test samples to the data sets already stored in a database.

Monitoring the expression of a large number of genes in several samples leads to the generation of a large amount of data that is too complex to be easily interpreted. Several unsupervised and supervised multivariate data analysis techniques have already been shown to be useful in extracting meaningful biological information from these large data sets. Cluster analysis is by far the most commonly used technique for gene expression analysis, and has been performed to identify genes that are regulated in a similar manner, and or identifying new/unknown tumour classes using gene expression profiles (Eisen et al., 1998, PNAS, 95, p14863-14868, Alizadeh et al. 2000, supra, Perou et al. 2000, Nature, 406, p747-752; Ross et al, 2000, Nature Genetics, 24(3), p227-235; Herwig et al., 1999, Genome Res., 9, p1093-1105; Tamayo et al, 1999, Science, PNAS, 96, p2907-2912).

In the clustering method, genes are grouped into functional categories (clusters) based on their expression profile, satisfying two criteria: *homogeneity*

- the genes in the same cluster are highly similar in expression to each other; and *separation* - genes in different clusters have low similarity in expression to each other.

Examples of various clustering techniques that have been used for gene expression analysis include hierarchical clustering (Eisen et al., 1998, supra; Alizadeh et al. 2000, supra; Perou et al. 2000, supra; Ross et al, 2000, supra), K-means clustering (Herwig et al., 1999, supra; Tavazoie et al, 1999, Nature Genetics, 22(3), p. 281-285), gene shaving (Hastie et al., 2000, Genome Biology, 1(2), research 0003.1-0003.21), block clustering (Tibshirani et al., 1999, Tech repot Univ Stanford.) Plaid model (Lazzeroni, 2002, Stat. Sinica, 12, p61-86), and self-organizing maps (Tamayo et al. 1999, supra). Also, related methods of multivariate statistical analysis, such as those using the singular value decomposition (Alter et al., 2000, PNAS, 97(18), p10101-10106; Ross et al. 2000, supra) or multidimensional scaling can be effective at reducing the dimensions of the objects under study.

However, methods such as cluster analysis and singular value decomposition are purely exploratory and only provide a broad overview of the internal structure present in the data. They are unsupervised approaches in which the available information concerning the nature of the class under investigation is not used in the analysis. Often, the nature of the biological perturbation to which a particular sample has been subjected is known. For example, it is sometimes known whether the sample whose gene expression pattern is being analysed derives from a diseased or healthy individual. In such instances, discriminant analysis can be used for classifying samples into various groups based on their gene expression data.

In such an analysis one builds the classifier by training the data that is capable of discriminating

between member and non-members of a given class. The trained classifier can then be used to predict the class of unknown samples. Examples of discrimination methods that have been described in the literature include Support Vector Machines (Brown et al, 2000, PNAS, 97, p262-267), Nearest Neighbour (Dudoit et al., 2000, supra), Classification trees (Dudoit et al., 2000, supra), Voted classification (Dudoit et al., 2000, supra), Weighted Gene voting (Golub et al. 1999, supra), and Bayesian classification (Keller et al. 2000, Tec report Univ of Washington). Also a technique in which PLS (Partial Least Square) regression analysis is first used to reduce the dimensions in the gene expression data set followed by classification using logistic discriminant analysis and quadratic discriminant analysis (LD and QDA) has recently been described (Nguyen & Rocke, 2002, Bioinformatics, 18, p39-50 and 1216-1226).

A challenge that gene expression data poses to classical discriminatory methods is that the number of genes whose expression are being analysed is very large compared to the number of samples being analysed. However in most cases only a small fraction of these genes are informative in discriminant analysis problems. Moreover, there is a danger that the noise from irrelevant genes can mask or distort the information from the informative genes. Several methods have been suggested in literature to identify and select genes that are informative in microarray studies, for example, t-statistics (Dudoit et al, 2002, J. Am. Stat. Ass., 97, p77-87), analysis of variance (Kerr et al., 2000, PNAS, 98, p8961-8965), Neighbourhood analysis (Golub et al, 1999, supra), Ratio of between groups to within groups sum of squares (Dudoit et al., 2002, supra), Non parametric scoring (Park et al., 2002, Pacific Symposium on Biocomputing, p52-63) and Likelihood selection (Keller et al., 2000, supra).

In the methods described herein the gene expression data that has been normalized and standardized is analysed by using Partial Least Squares Regression (PLSR). Although PLSR is primarily a method used for regression analysis of continuous data (see Appendix A), it can also be utilized as a method for model building and discriminant analysis using a dummy response matrix based on a binary coding. The class assignment is based on a simple dichotomous distinction such as breast cancer (class 1) / healthy (class 2), or a multiple distinction based on multiple disease diagnosis such as breast cancer (class 1) / Alzheimer (class 2) / healthy (class 3). The list of diseases for classification can be increased depending upon the samples available corresponding to other diseases or conditions or stages thereof.

PLSR applied as a classification method is referred to as PLS-DA (DA standing for Discriminant analysis). PLS-DA is an extension of the PLSR algorithm in which the Y-matrix is a dummy matrix containing n rows (corresponding to the number of samples) and K columns (corresponding to the number of classes). The Y-matrix is constructed by inserting 1 in the kth column and -1 in all the other columns if the corresponding ith object of X belongs to class k. By regressing Y onto X, classification of a new sample is achieved by selecting the group corresponding to the largest component of the fitted, $\hat{y}(x) = (\hat{y}_1(x), \hat{y}_2(x), \ldots, \hat{y}_k(x))$. Thus, in a -1/1 response matrix, a prediction value below 0 means that the sample belongs to the class designated as -1, while a prediction value above 0 implies that the sample belongs to the class designated as 1.

An advantage of PLSR-DA is that the results obtained can be easily represented in the form of two different plots, the score and loading plots. Score plots represent a projection of the samples onto the principal components and shows the distribution of the

samples in the classification model and their relationship to one another. Loading plots display correlations between the variables present in the data set.

It is usually recommended to use PLS-DA as a starting point for the classification problem due to its ability to handle collinear data, and the property of PLSR as a dimension reduction technique. Once this purpose has been satisfied, it is possible to use other methods such as Linear discriminant analysis, LDA, that has been shown to be effective in extracting further information, Indahl et al. (1999, Chem. and Intell. Lab. Syst., 49, p19-31). This approach is based on first decomposing the data using PLS-DA, and then using the scores vectors (instead of the original variables) as input to LDA. Further details on LDA can be found in Duda and Hart (Classification and Scene Analysis, 1973, Wiley, USA).

The next step following model building is of model validation. This step is considered to be amongst the most important aspects of multivariate analysis, and tests the "goodness" of the calibration model which has been built. In this work, a cross validation approach has been used for validation. In this approach, one or a few samples are kept out in each segment while the model is built using a full cross-validation on the basis of the remaining data. The samples left out are then used for prediction/classification. Repeating the simple cross-validation process several times holding different samples out for each cross-validation leads to a so-called double cross-validation procedure. This approach has been shown to work well with a limited amount of data, as is the case in some of the Examples described here. Also, since the cross validation step is repeated several times the dangers of model bias and overfitting are reduced.

Once a calibration model has been built and

validated, genes exhibiting an expression pattern that is most relevant for describing the desired information in the model can be selected by techniques described in the prior art for variable selection, as mentioned elsewhere. Variable selection will help in reducing the final model complexity, provide a parsimonious model, and thus lead to a reliable model that can be used for prediction. Moreover, use of fewer genes for the purpose of providing diagnosis will reduce the cost of the diagnostic product. In this way informative probes which would bind to the genes of relevance may be identified.

We have found that after a calibration model has been built, statistical techniques like Jackknife (Effron, 1982, The Jackknife, the Bootstrap and other resampling plans. Society for Industrial and Applied mathematics, Philadelphia, USA), based on resampling methodology, can be efficiently used to select or confirm significant variables (informative probes).

The approximate uncertainty variance of the PLS regression coefficients B can be estimated by:

$$S^2B = \sum_{m=1}^{M} ((B-B_m)g)^2$$

where

S^2B = estimated uncertainty variance of B;

B = the regression coefficient at the cross validated rank A using all the N objects;

B_m = the regression coefficient at the rank A using all objects except the object(s) left out in cross validation segment m; and

g = scaling coefficient (here: g=1).

In our approach, Jackknife has been implemented together with cross-validation. For each variable the difference between the B-coefficients B_i in a

cross-validated sub-model and B_{tot} for the total model is first calculated. The sum of the squares of the differences is then calculated in all sub-models to obtain an expression of the variance of the B_i estimate for a variable. The significance of the estimate of B_i is calculated using the t-test. Thus, the resulting regression coefficients can be presented with uncertainty limits that correspond to 2 Standard Deviations, and from that significant variables are detected.

No further details as to the implementation or use of this step are provided here since this has been implemented in commercially available software, The Unscrambler, CAMO ASA, Norway. Also, details on variable selection using Jackknife can be found in Westad & Martens (2000, J. Near Inf. Spectr., 8, p117-124).

The following approach can be used to select informative probes from a gene expression data set:

a) keep out one unique sample (including its repetitions if present in the data set) per cross validation segment;

b) build a calibration model (cross validated segment) on the remaining samples using PLSR-DA;

c) select the significant genes for the model in step b) using the Jackknife criterion;

d) repeat the above 3 steps until all the unique samples in the data set are kept out once (as described in step a). For example, if 75 unique samples are present in the data set, 75 different calibration models are built resulting in a collection of 75 different sets of significant probes;

e) select the most significant variables using the frequency of occurrence criterion in the generated sets of significant probes in step d). For example, a set of probes appearing in all sets (100%) are more informative than probes appearing in only 50% of the

generated sets in step d).

Once the informative probes for a disease have been selected, a final model is made and validated. The two most commonly used ways of validating the model are cross-validation (CV) and test set validation. In cross-validation, the data is divided into k subsets. The model is then trained k times, each time leaving out one of the subsets from training, but using only the omitted subset to compute error criterion, RMSEP (Root Mean Square Error of Prediction). If k equals the sample size, this is called "leave-one-out" cross-validation. The idea of leaving one or a few samples out per validation segment is valid only in cases where the covariance between the various experiments is zero. Thus, one sample at-a-time approach can not be justified in situations containing replicates since keeping only one of the replicates out will introduce a systematic bias in our analysis. The correct approach in this case will be to leave out all replicates of the same samples at a time since that would satisfy assumptions of zero covariance between the CV-segments.

The second approach for model validation is to use a separate test-set for validating the calibration model. This requires running a separate set of experiments to be used as a test set. This is the preferred approach given that real test data are available.

The final model is then used to identify a disease, condition or stage thereof in test samples. For this purpose, expression data of selected informative genes is generated from test samples and then the final model is used to determine whether a sample belongs to a diseased or non-diseased class or has a condition or stage thereof.

Thus viewed from a yet further aspect the present invention provides a method of identifying probes useful for diagnosing or identifying or monitoring a disease or

condition or stage thereof in an organism, comprising the steps of:

a) immobilizing a set of oligonucleotide probes, preferably as described hereinbefore, on a solid support;

b) isolating mRNA from a sample of a normal organism (normal sample), which may optionally be reverse transcribed to cDNA;

c) isolating mRNA from a sample from an organism, corresponding to the sample and organism of step (b), which is known to have said disease or condition or a stage thereof (diseased sample), which may optionally be reverse transcribed to cDNA;

d) hybridizing the mRNA or cDNA of steps (b) and (c) to said set of immobilized oligonucleotide probes of step (a); and

e) assessing the amount of mRNA or cDNA hybridizing to each of said oligonucleotide probes to determine the level of gene expression of genes to which said oligonucleotide probes bind in said normal and diseased samples to generate a gene expression data set for each sample;

f) normalizing and standardizing said data set of step (e);

g) constructing a calibration model for classification, preferably using the statistical techniques Partial Least Squares Discriminant Analysis (PLS-DA) and Linear Discriminant Analysis (LDA);

h) performing JackKnife analysis and identifying those oligonucleotide probes which are required for classification of said disease and normal samples into their respective groups.

Preferably a model for classification purposes is

generated by using the data relating to the probes identified according to the above described method. Preferably the sample is as described previously. Preferably the oligonucleotides which are immobilized in step (a) are randomly selected as described below or are the probes as described hereinbefore. Such oligonucleotides may be of considerable length, e.g. if using cDNA (which is encompassed within the scope of the term "oligonucleotide"). The identification of such cDNA molecules as useful probes allows the development of shorter oligonucleotides which reflect the specificity of the cDNA molecules but are easier to manufacture and manipulate.

The above described model may then be used to generate and analyse data of test samples and thus may be used for the diagnostic methods of the invention. In such methods the data generated from the test sample provides the gene expression data set and this is normalized and standardized as described above. This is then fitted to the calibration model described above to provide classification.

The method described herein can also be used to simultaneously select informative probes for several related and unrelated diseases or conditions. Depending upon which diseases or conditions have been included in the calibration or training set, informative probes can be selected for the said diseases or conditions. The informative probes selected for one disease or condition may or may not be similar to the informative probes selected for another disease or condition of interest. It is the pattern with which the selected genes are expressed in relation to each other during a disease, condition, or stage thereof, that determines whether or not they are informative for the disease, condition or stage thereof.

In other words, informative genes are selected based on how their expression correlates with the

expression of other selected informative genes under the influence of responses generated by the disease, condition or stage thereof under investigation. In examples 1 and 2 provided hereinafter, 139 informative probes were selected for breast cancer diagnosis and 182 probes were selected for Alzheimer's disease diagnosis by training the gene expression data set of genes representing 1435 or 758 randomly picked cDNA clones for breast cancer/non breast cancer samples, or Alzheimer/non-Alzheimer samples, respectively. Among the probes selected for breast cancer and Alzheimer, about 10 probes were informative both for breast cancer and Alzheimer disease diagnosis.

For the purpose of isolating informative probes or identifying several related and unrelated diseases, conditions and stages thereof simultaneously, the gene expression data set must contain the information on how genes are expressed when the subject has a particular disease, condition or stage thereof under investigation. The data set is generated from a set of healthy or diseased samples, where a particular sample may contain the information of only one disease, condition or stages thereof or may also contain information about multiple diseases, conditions or stages thereof. For example, if the isolation of informative probes for Alzheimer disease, breast cancer and diabetes is sought, whole blood samples can be obtained from an Alzheimer patient who has breast cancer and diabetes. Hence, the method also teaches an efficient experimental design to reduce the number of samples required for isolating informative probes by selecting samples representing more than one disease, condition or stage thereof.

As mentioned previously, in view of the high information content of most transcripts, the identification and selection of informative probes for use in diagnosing, monitoring or identifying a particular disease, condition or stage thereof may be

dramatically simplified. Thus the pool of genes from which a selection may be made to identify informative probes may be radically reduced.

Unlike, in prior art technologies where informative probes are selected from a population of thousands of genes that are being expressed in a cell, like in microarray, in the method described herein, the informative probes are selected from a limited number of randomly obtained genes. For example, from a population of 1435 cDNA clones, randomly picked from a human whole blood cDNA library, we were able to select 139 informative probes for breast cancer diagnosis (see Example 1 and Table 2).

Thus in a preferred aspect of the above mentioned method of identifying probes useful for diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, said set of oligonucleotides which are immobilized in step (a) are randomly selected from a larger set of oligonucleotides, e.g. from a cDNA library or other oligonucleotide pool, which may be, but is preferably not selected from the set provided herein. Preferably said larger set comprises oligonucleotides which correspond to moderately or highly expressed genes. Thus preferably in methods of the invention, the set of oligonucleotides according to the invention are replaced with a set of oligonucleotides which are randomly selected, e.g. from commercially available oligonucleotide or cDNA libraries.

As referred to herein "random" refers to selection which is not biased based on the extent of information carried by the transcripts in relation to the disease, condition or organism under study, ie. without bias towards their likely utility as informative probes. Whilst a random selection may be made from a pool of transcripts (or related products) which have been biased, e.g. to highly or moderately expressed

transcripts, preferably random selection is made from a pool of transcripts not biased or selected by a sequence-based criterion. The larger set may therefore contain oligonucleotides corresponding to highly and moderately expressed genes, or alternatively, may be enriched for those corresponding to the highly and moderately expressed genes.

Random selection from highly and moderately expressed genes can be achieved in a wide variety of ways. A strategy used in this work, but not limiting in itself involves randomly picking a significant number of cDNA clones from a cDNA library constructed from a biological specimen under investigation. Since, in a cDNA library, the cDNA clones corresponding to transcripts present in high or moderate amount are more frequently present than transcripts corresponding to cDNA present in low amount, the former will tend to be picked up more frequently than the latter. A pool of cDNA enriched for those corresponding to highly and moderately expressed genes can be isolated by this approach.

To identify genes that are expressed in high or moderate amount among the isolated population for use in methods of the invention, the information about the relative level of their transcripts in samples of interest can be generated using several prior art techniques. Both non-sequence based methods, such as differential display or RNA fingerprinting, and sequence-based methods such as microarrays or macroarrays can be used for the purpose. Alternatively, specific primer sequences for highly and moderately expressed genes can be designed and methods such as quantitative RT-PCR can be used to determine the levels of highly and moderately expressed genes. Hence, a skilled practitioner may use a variety of techniques which are known in the art for determining the relative level of mRNA in a biological sample.

Especially preferably the sample for the isolation of mRNA in the above described method is as described previously and is preferably not from the site of disease and the cells in said sample are not disease cells and have not contacted disease cells.

The following examples are given by way of illustration only in which the Figures referred to are as follows:

Figure 1 shows the effect of Direct Standardization (DS) on the Alzheimer data measured in two different series of experiments in which AD denotes Alzheimer's samples and A,B are non-Alzheimer's samples. The samples in both series have been labelled systematically as (xx_7/xx_8), whereas the corrected samples from series 8 (in b,c,d) have been labelled as (xx_c), thus, for example, AD2-7 denotes Alzheimer disease sample number 2 in experiment series 7. The circled spots represent the samples chosen as the transfer samples. The connecting lines in figures b,c,d show the proximity of the replicated samples after applying DS. The dashed lines in figures a,c,d represent the decision boundary separating the classes. These lines have not been drawn on the basis of any statistical criteria, but serve the purpose of visually separating the classes. All the four figures show scores plot (PC1-PC2) from PCA analysis based on (a) non-standardized data, (b) scores plot after direct standardization using 3 transfer samples, (c) scores plot after direct standardization using 4 transfer sample, (d) scores plot after direct standardization using 8 transfer samples;

Figure 2 shows the projection of normal (including benign) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 44 informative genes, in which PC is the principal components and N and C are normal and breast cancer samples, respectively;

Figure 3 shows the projection of individuals with

and without Alzheimer's disease onto a classification model generated by PLSR-DA using 182 informative genes;

Figures 4, 6 and 8 show projection plots as Figure 2 in which the classification model is generated using 719, 111 and 345 cDNAs, respectively, wherein PC is the principal components, N denotes normal and B denotes breast cancer samples;

Figures 5, 7 and 9 show prediction plots based on 3 principal components using the data of 719, 111 and 345 cDNAs, respectively;

Figure 10 shows a projection plot as Figure 3 in which the classification model is generated using 520 cDNAs; and

Figure 11 is the prediction plot corresponding to Figure 10.

Example 1: Diagnosis of Breast Cancer

Methods

Whole blood was obtained from the arms of breast cancer patients and patients with benign tumours (Ullevål and Haukland hospitals in Norway). All of the patients with breast cancer had a malignant tumour of the breast (disease samples). Healthy blood was collected from the above two hospitals, or collected at a Health station at Ås, Norway or at DiaGenic AS, Norway, from the arms of female donors with no reported signs of breast cancer. The blood from healthy individuals or with benign tumours comprise the normal samples. The blood was either collected in tubes containing EDTA and stored immediately at -80^{0}C or was collected in PAXgene tubes and stored for 12-24 hours at room temperature before finally storing them at -80^{0}C before use. Further details of the breast cancer and benign tumour patients from which blood was taken is provided in Table 5.

mRNA was isolated from the blood of the 29 breast cancer patients and 46 normal donors and used to prepare labelled probes by reverse transcribing in the presence of $\alpha^{33}P$-dATP. The first strand cDNA of the normal and diseased samples was bound, separately to 1435 cDNA clones immobilized on a solid support (nylon membrane). These cDNA clones were randomly picked, without any prior knowledge of their gene sequences, from a cDNA library constructed using whole blood of 550 healthy individuals (Clontech, Palo Alto, USA). These methods were conducted as follows.

For amplification of inserts, bacterial clones were grown in microtiter plates containing 150 μl LB with 50 μg/ml carbenicillin, and incubated overnight with agitation at 37°C. To lyse the cells, 5 μl of each culture were diluted with 50 μl H2O and incubated for 12 min. at 95°C. Of this mixture, 2 μl were subjected to a PCR reaction using 20 pmoles of M13 forward and reverse primer in presence of 1.5 mM $MgCl_2$. PCR reactions were performed with the following cycling protocol: 4 min. at 95°C, followed by 25 cycles of 1 min. at 94°C, 1 min. at 60°C and 3 min. at 72°C either in a RoboCycler® Temperature Cycler (Stratagene, La Jolla, USA) or DNA Engine Dyad Peltier Thermal Cycler (MJ Research Inc., Waltham, USA). The amplified products were denatured by incubating with NaOH (0.2 M, final concentration) for 30 min. and spotted onto Hybond-N+ membranes (Amersham Pharmacia Biotech, Little Chalfont, UK), using MicroGrid II workstation according to the manufacturer's instructions (BioRobotics Ltd, Cambridge England). The immobilized cDNAs were fixed using a UV cross-linker (Hoefer Scientific Instruments, San Francisco, USA).

In addition to the 1435 cDNAs, the printed arrays also contained controls for assessing background level, consistency and sensitivity of the assay. These were

spotted at multiple positions and included controls such as PCR mix (without any insert); positive and negative controls of SpotReportTM 10 array validation system (Stratagene, La Jolla, USA) and cDNAs corresponding to constitutively expressed genes such as b-actin, g-actin, GAPDH, HOD and cyclophilin. Also, oligonucleotides corresponding to SIX1, b-tubulin, TRP-2, MDM2, Myosin Light C, CD44, Maspin, Laminin, and SRP 19 were included to detect disseminated cancer cells.

The total RNA from blood collected in EDTA tubes was purified using Trizol LS Reagent protocol (Invitrogen/Life Technologies). From blood contained in PAXgene tubes, the total RNA was purified according to the supplier's instructions (PreAnalytiX, Hombrechtikon, Switzerland). Contaminating DNA was removed from the isolated RNA by DNAase I treatment using DNA-free kit (Ambion, Inc. Austin, USA). RNA quality was determined visually by inspecting the integrity of 28S and 18S ribosomal bands following agarose gel electrophoresis. The concentration and purity of extracted RNA was determined by measuring the absorbance at 260 nm and 280 nm. mRNA was isolated from the total RNA using Dynabeads as per the supplier's instructions (Dynal AS, Oslo, Norway).

Labelling and hybridization experiments were performed in batches. The number of samples assayed in each batch varied from six to nine. In the case of samples that were assayed more than once (replicates), aliquots derived from the same mRNA pool were used for probe synthesis. For probe synthesis, aliquots of mRNA corresponding to 4-5 μg of total RNA were mixed together with oligodT_{25NV} (0.5 μg/ml) and mRNA spikes of SpotReport™ 10 array validation system (10 pg; Spike 2, 1 pg), heated to 70°C to remove secondary structures, and then chilled on ice. Probes were prepared in 35μl

reaction mixes by reverse transcription in the presence of 50μCi [α^{33}P] dATP, 3.5 μM dATP, 0.6 mM each of dCTP, dTTP, dGTP, 200 units of SuperScript reverse transcriptase (Invitrogen, LifeTechnologies) and 0.1 M DTT, labelling for 1.5 hr at 42°C. Following synthesis, the enzyme was deactivated for 10 min. at 70°C and mRNA removed by incubating the reaction mix for 20 min. at 37°C in 4 units of Ribo H (Promega, Madison USA). Unincorporated nucleotides were removed using ProbeQuant G 50 Columns (Amersham Biosciences, Piscataway, USA).

Prior to hybridization, the membranes were equilibrated in 4 x SSC for 2 hr at room temperature and prehybridized overnight at 65°C in 10 ml prehybridisation solution (4 x SSC, 0.1 M NaH_2PO_4, 1 mM EDTA, 8% dextran sulphate, 10 x denhardt's solution, 1% SDS). Freshly prepared probes were added to 5 ml of the same prehybridisation solution, and hybridization continued overnight at 65°C. The membranes were washed at 65°C at increasing stringency (2 x 30 min. each in 2 x SSC, 0.1% SDS; 1 x SSC, 0.1% SDS; 0.1 x SSC, 0.1% SDS) to remove unspecific signals.

The amount of labelled first strand cDNA binding to each spot was assessed and quantified using a PhosphoImager to generate a gene expression data set. The data was generated using Phoretix software version 3 (Non Linear Dynamics, England). Background subtraction was performed on the generated data by subtracting the median of the line of pixels around each spot outline from the total intensity obtained from the respective spots.

The background-subtracted data was then normalized and transformed by selecting out 50 lowest and 50 maximum signals from each membrane. This step was to exclude genes that were expressed with a high degree of

variance. Since the genes varied from membrane to membrane, the expression data from 497 genes were removed from the data set. The values for the remaining 938 genes were then normalised by using different approaches such as external controls, dividing each spot by the median intensity of the observed signal in the respective membrane, range normalizing the data from each membrane, and then log transforming the data obtained.

The processed data obtained above was then used to isolate the informative probes by:

a) keeping one unique sample (including all repetitions of the selected sample) out per cross validation segment;

b) building a calibration model (cross validated) on the remaining samples using PLSR-DA;

c) selecting the set of significant genes for the model in step b using the Jackknife criterion;

d) repeating steps a), b) and c) until all the unique samples were kept out once (hence, in all 75 different calibration models were built (after repeating step b) 75 times), resulting in 75 different sets of significant probes (after repeating step c) 75 times));

e) selecting significant variables using the frequency of occurrence criterion amongst the 75 different sets of significant probes.

The selected informative probes based on occurrence criterion were used to construct a classification model. The result of the classification model based on probes appearing in at least 90% of the generated sets after the step of isolating informative probes as described above is shown in Figure 2 in which it is seen that the expression pattern of these genes was able to classify most women with breast cancer and women with no breast cancer into distinct groups. In this figure PC1 and PC2

indicate the two principal components statistically derived from the data which best define the systemic variability present in the data. This allows each sample, and the data from each of the informative probes to which the sample's labelled first strand cDNA was bound, to be represented on the classification model as a single point which is a projection of the sample onto the principal components - the score plot.

The ability of the generated model, based on isolated informative probes, to predict future samples was determined by the double cross-validation approach. The performance of the diagnostic test for breast cancer based on the occurrence criterion is presented in Table 6.

Correct prediction of most breast cancer cells was achieved. These included all three samples obtained from women with ductal carcinoma in situ (DCIS), 11/15 samples obtained from women with stage I breast cancer, all five samples obtained from women with stage II breast cancer, and one of two samples obtained from women with stage III breast cancer. Interestingly, two correctly predicted stage I samples were obtained from women having a tumour size of <5 mm in diameter.

The model also correctly predicted the class of most non-cancer samples (41/46), including those that were obtained from women with non-cancerous breast abnormalities.

Confirmation that the gene transcripts are not from cells which are disseminated disease cells has been confirmed by several lines of evidences. Firstly, the informative genes were expressed constitutively at high or moderate levels in blood cells of women irrespective of whether they had cancer or not. Secondly, in the

assay described in this Example, in order to identify transcripts, at least 720 disseminated cells in blood samples would be required. Since, the average number of disseminated cells present in blood during different stages of breast cancer is much lower (organ confined breast cancer, 0.8 cells per ml; invasive breast cancer spread to lymph nodes only, 2.4 cells per ml; and metastatic breast cancer, 6 cells per ml; SD>100%) (29), we believe that the signals being detected originated from peripheral blood cells and could not have originated from disseminated cells. Thirdly, we were not able to detect any signal from the eight cancer markers known to have elevated expression in malignant cancer cells, including cancer cells that are disseminated in the blood.

Example 2: Diagnosis of Alzheimer's disease

Similar experiments were conducted with samples from Alzheimer's patients. In this method 7 patients diagnosed with Alzheimer's Disease at the Memory Clinic at Ullevål University Hospital were used in the trial. The patients were confirmed as having Alzheimer's disease based on the following criteria:

* A standardized interview with a care-giver using IQCODE, an ADL scale and a scale measuring behaviour of the patient (Green scale).
* Neuropsychological evaluation using MMSE, Clock drawing test, Trailmaking test A and B (TMT A and B), Kendrick object learning test (visual memory test), part of the Wechsler battery and Benton test.
* A psychiatric evaluation using scales for detection of depression, MADRS for interviewing the patient and Cornell scale for interviewing the care-giver.
* A physical examination.
* Laboratory tests of blood samples to rule out other

diseases.

* CT scan of the brain.
* SPECT of the brain.

The mean age of the patients was 72.3 with an age range of 69-76. The mean MMSE score was 22.0 (the maximum score attainable being 30).

Six age-matched individuals without diagnosed Alzheimer's disease were used as a control. All had been tested with MMSE and had a minimum score of 28 (mean: 28.4). The mean age of the normal control group was 73.0 and the age range 66-81. A sample from a 16-year old individual, with a consequent minimal chance of having Alzheimer's disease, was also included as an additional control.

Using the methods described above (except that hybridization to 758 rather than 1435 cDNA clones was performed), informative probes were selected based on occurrence criterion and used to construct a classification model. The results of the classification model based on probes appearing at least once in the generated sets after the method to isolate informative probes as described above is shown in Figure 3 in which it will be seen that the expression pattern of these genes was able to classify individuals with or without Alzheimer's disease into distinct groups. In this Figure PC1 and PC2 indicate the 2 principal components statistically derived from the data which define the systematic variability present in the data. This allows each sample, and the data from each of the informative probes to which the samples' cDNA was bound, to be represented on the classification model as a single point which is a projection of the sample onto the principal components - the score plot.

The ability of the generated model, based on isolated informative probes, to predict future samples was determined by the double cross-validation. The performance of the diagnostic test for Alzheimer's disease is presented in Table 7.

Appendix A

Partial Least Squares regression (PLSR)

Let a multivariate regression model be defined as:

$Y = XB + F$

where

X a $N x P$ matrix with N predictor variables (genes);
Y ($N x J$) being the J predicted variables. In our case Y represents a matrix containing dummy variables;
B is a matrix of regression coefficients; and
F is a $N x J$ matrix of residuals.

The structure of the PLSR model can be written as:

$X = TP^T + E_A$, and
$Y = TQ^T + F_A$, where

where
T ($N x A$) is a matrix of score vectors which are linear combinations of the x-variables;
P ($P x A$) is a matrix with the x-loading vectors p_a as columns;
Q ($J x A$) is a matrix with the y-loading vectors q_a as columns;
E_a ($N x P$) is the matrix for X after A factors; and
F_a ($N x J$) is the matrix for Y after A factors.

The criterion in PLSR is to maximize the explained covariance of [X,Y]. This is achieved by the loading weights vector w_{a+1}, which is the first eigenvector of $E_a^T F_a F_a^T E_a$ (E_a and F_a are the deflated X and Y after a factors or PLS components).

The regression coefficients are given by:

$$B = W(P^T W)^{-1} Q^T$$

A PLSR model with full rank, i.e. maximum number of components, is equivalent to the MLR solutions. Further details on PLSR can be found in Marteus & Naes, 1989, Multivariate Calibration, John Wiley & Sons, Inc., USA and Kowalski & Seasholtz, 1991, supra.

Example 3: Validation of Example 1, diagnosis of breast cancer

The results in Example 1 were validated by using the informative probes identified in Example 1 on new beast cancer and control samples.

Methods

The methods, essentially as described in Example 1, were used. Blood was taken from patients as described in Table 8. However, blood was collected in PAXgene tubes and the first strand labelled cDNAs were hybridized to 719 cDNAs spotted on nylon membranes along with other controls as described in Example 1. After background subtraction using control spots, the data of each membrane was normalized using the inter quantile range. The data was analysed as described in Example 1 and the model validated by cross validation.

The 719 cDNAs which were spotted are a subset of the cDNAs spotted in Example 1 and include 111 cDNAs described in Table 2 and which were found to be informative in Example 1.

Results

The results are shown in Figures 4 to 9. Figures 4, 6 and 8 are projection plots similar to Figure 2 and show the projection of normal and breast cancer patients' samples onto a classification model generated using all 719 cDNA. Figure 6 is similar but uses a classification model generated with the 111 probes common to Example 1. Figure 8 uses the 345 sequences of the 719 for which sequence information is provided herein. In each case classification of normal and breast cancer groups was possible. Figures 5, 7 and 9 show prediction plots which reflect the ability of the generated models to correctly diagnose breast cancer. In the 3 prediction

plots shown, the disease samples appear on the x axis at +1 and the non-disease samples appear at -1. The y axis represents the predicted class membership. During prediction, if the prediction is correct, disease samples should fall above zero and non-disease samples should fall below zero. In each case almost all samples are correctly predicted.

<u>Example 4: Validation of Example 2, diagnosis of Alzheimers</u>

The results in Example 2 were validated by using the informative probes identified in Example 2 on new Alzheimer's patient samples.

<u>Methods</u>

The methods, essentially as described in Example 2, were used. Twelve female patients diagnosed with Alzheimer's disease at the Memory Clinic at Ullevål University Hospital who were confirmed as having Alzheimer's disease based on the criteria of Example 2 were used in the trial. The mean age of the patients was 72.3 with an age range of 66-83. The mean MMSE score was 22.0 (the maximum score attainable being 30).

Sixteen age-matched female individuals without diagnosed Alzheimer's disease were used as the normal control group. All had been tested with MMSE and had a minimum score of 29. The mean age of the normal control group was 74.0 and the age range 66-86.

After transfer of the blood to PAXgene tubes, total mRNA was isolated from the blood of the Alzheimer's disease and from the control group donors according to the manufacturers's instructions (PreAnalytiX, Hombrechtikon, Switzerland). The isolated mRNA was labelled during reverse transcription in the presence of

α^{33}P-dATP, yielding a labelled first strand cDNA. Hybridization was performed as described previously onto 730 cDNA clones picked from a cDNA library from whole blood of 550 healthy individuals without knowledge of the gene sequence of the random cDNA clones.

Results

The results are shown in Figures 10 and 11. Figure 10 is a projection plot generated using 520 probes which have been sequenced. Figure 11 is a prediction plot and shows correct prediction of almost all samples.

Table 1a

List of probes informative for disease diagnosis

	Clone ID	Sequence ID	No. of nucleotides
1	I-01	-	-
2	I-02	-	-
3	I-13	-	-
4	I-21	-	-
5	I-24	308	373
6	I-28	310	564
7	I-30	1180	622
8	I-34	313	554
9	I-37	-	-
10	I-42	-	-
11	I-52	-	-
12	I-54	1181	155
13	I-58	326	554
14	I-71	-	-
15	I-72	-	-
16	I-86	-	-
17	I-95	-	-
18	II-03	361	622
19	II-05	363	628
20	II-06	364	528
21	II-10	368	329
22	II-24	381	534
23	II-25	382	444
24	II-26	383	566
25	II-33	390	523
26	II-34	391	566
27	II-41	397	534
28	II-42	398	512
29	II-47	-	-
30	II-57	411	505
31	II-61	415	596
32	II-69	423	387
33	II-70	424	420
34	II-75	429	535
35	II-83	-	-
36	II-84	438	577
37	II-87	441	552
38	II-88	442	606
39	II-90	-	-
40	II-94	448	329
41	III-02	453	747
42	III-05	-	-
43	III-06	458	682

44	III-08	460	536
45	III-10	-	-
46	III-13	464	615
47	III-15	-	-
48	III-17	-	-
49	III-20	1183	479
50	III-23	473	694
51	III-26	476	476
52	III-35	485	551
53	III-39	487	224
54	III-40	488	349
55	III-43	490	382
56	III-44	491	382
57	III-53	500	390
58	III-56	503	109
59	III-57	504	374
60	III-60	-	-
61	III-60	-	-
62	III-61	507	521
63	III-63	509	575
64	III-68	-	-
65	III-74	518	502
66	III-80	523	585
67	III-82	-	-
68	III-85	526	516
69	III-89	530	660
70	III-92	-	-
71	III-96	-	-
72	IV-14	684	545
73	IV-15	1185	628
74	IV-23	-	-
76	IV-26	1186	494
75	IV-26	-	-
77	IV-29	-	-
78	IV-31	687	268
79	IV-32	688	569
80	IV-34	-	-
81	IV-35	-	-
82	IV-41	-	-
83	IV-45	-	-
84	IV-53	61	362
85	IV-62	-	-
86	IV-69	192	286
87	IV-80	701	579
88	IV-82	-	-
89	IV-93	-	-
90	IX-10	736	641
91	IX-12	-	-
92	IX-38	757	583
93	IX-39	758	424
94	IX-42	-	-
95	IX-48	764	626
96	IX-77	785	556
97	V-01	-	-
98	V-02	-	-
99	V-03	706	496

100	V-04	707	397
101	V-06	-	-
102	V-07	708	293
103	V-11	1188	599
104	V-12	711	498
105	V-15	-	-
106	V-17	-	-
107	V-21	-	-
108	V-25	-	-
109	V-32	-	-
110	V-35	-	-
111	V-39	-	-
112	V-42	-	-
113	V-43	-	-
114	V-47	-	-
115	V-49	-	-
116	V-52	-	-
117	V-54	-	-
118	V-55	77	412
119	V-58	-	-
120	V-59	-	-
121	V-65	-	-
122	V-68	-	-
123	V-71	-	-
124	V-75	-	-
125	V-79	-	-
126	V-80	726	260
127	V-90	-	-
128	V-91	-	-
129	V-92	-	-
130	V-94	-	-
131	VI-02	-	-
132	VI-04	865	122
133	VI-07	93	405
134	VI-09	-	-
135	VI-10	-	-
136	VI-12	869	667
137	VI-14	871	642
138	VI-17	-	-
139	VI-20	876	115
140	VI-21	-	-
141	VI-23	878	634
142	VI-34	-	-
143	VI-41	-	-
144	VI-42	-	-
145	VI-43	-	-
146	VI-44	-	-
147	VI-48	891	626
148	VI-49	-	-
149	VI-50	893	585
150	VI-52	-	-
151	VI-53	895	560
152	VI-55	897	509
153	VI-65	-	-
154	VI-70	108	550
155	VI-71	-	-

156	VI-72	-	-
157	VI-74	905	655
158	VI-76	907	582
159	VI-78	-	-
160	VI-79	-	-
161	VI-84	-	-
162	VI-87	911	595
163	VI-88	912	651
164	VI-90	-	-
165	VI-93	-	-
166	VI-95	915	230
167	VI-96	-	-
168	VII-02	-	-
169	VII-03	1196	412
170	VII-06	-	-
171	VII-10	-	-
172	VII-11	-	-
173	VII-15	1199	439
174	VII-19	562	580
175	VII-21	564	671
176	VII-25	-	-
177	VII-32	571	457
178	VII-36	575	209
179	VII-39	576	541
180	VII-42	579	502
181	VII-43	580	316
182	VII-46	583	631
183	VII-47	1200	526
184	VII-48	1201	613
185	VII-59	593	565
186	VII-60	-	-
187	VII-63	595	98
188	VII-66	598	362
189	VII-67	-	-
190	VII-72	600	595
191	VII-73	601	522
192	VII-75	-	-
193	VII-76	603	624
194	VII-77	1203	692
195	VII-80	605	338
196	VII-81	606	556
197	VII-83	-	-
198	VII-86	-	-
199	VII-88	-	-
200	VII-90	612	576
201	VII-91	613	341
202	VII-93	615	379
203	VIII-01	-	-
204	VIII-02	-	-
205	VIII-03	-	-
206	VIII-06	-	-
207	VIII-09	618	598
208	VIII-10	-	-
209	VIII-15	-	-
210	VIII-20	628	419
211	VIII-22	-	-

212	VIII-26	-	-
213	VIII-28	634	511
214	VIII-29	635	592
215	VIII-30	636	572
216	VIII-31	637	482
217	VIII-32	638	545
218	VIII-33	639	624
219	VIII-39	-	-
220	VIII-41	645	649
221	VIII-42	646	600
222	VIII-44	-	-
223	VIII-46	649	425
224	VIII-48	651	251
225	VIII-58	-	-
226	VIII-64	663	627
227	VIII-65	-	-
228	VIII-66	665	345
229	VIII-67	666	252
230	VIII-74	-	-
231	VIII-76	675	591
232	VIII-78	-	-
233	VIII-82	-	-
234	VIII-83	-	-
235	VIII-85	-	-
236	VIII-87	-	-
237	VIII-91	-	-
238	VIII-92	-	-
239	VIII-93	-	-
240	VIII-95	-	-
241	X-04	-	-
242	X-07	808	641
243	X-15	814	132
244	X-29	821	370
245	X-34	-	-
246	X-35	-	-
247	X-54	837	603
248	X-56	839	71
249	X-68	1207	642
250	X-72	849	622
251	X-94	860	501
252	XI-07	-	-
253	XI-13	1209	620
254	XI-50	-	-
255	XI-58	-	-
256	XI-81	1212	374
257	XII-07	1213	567
258	XII-17	-	-
259	XII-26	-	-
260	XII-27	-	-
261	XII-31	-	-
262	XII-32	-	-
263	XII-35	1214	620
264	XII-36	-	-
265	XII-52	-	-
266	XII-59	1216	484
267	XIII-19	1219	559

268	XIII-29	-	-
269	XIII-52	939	513
270	XIII-62	-	-
271	XIII-84	-	-
272	XIII-92	1221	741
273	XV-18	-	-
274	XV-22	1099	561
275	XV-24	-	-
276	XV-25	1224	485
277	XV-28	-	-
278	XV-34	-	-
279	XV-42	-	-
280	XV-68	-	-
281	XV-74	-	-
282	XV-93	-	-
283	XV-94	-	-
284	XV-96	-	-
285	XVI-36	1056	435
286	XVI-53	1230	741
287	XVI-59	-	-
288	XVI-66	1074	689
289	XVI-76	1083	198
290	XVI-77	1084	198
291	XVII-07	-	-
292	XVII-08	-	-
293	XVII-17	-	-
294	XVII-28	-	-
295	XVII-29	-	-
296	XVII-31	1139	503
297	XVII-36	-	-
298	XVII-39	-	-
299	XVII-40	1231	203
300	XVII-48	1148	587
301	XVII-55	-	-
302	XVII-58	-	-
303	XVII-67	-	-
304	XVII-72	-	-
305	XVII-76	1160	650
306	XVII-82	-	-
307	XVII-87	1165	502
308	XVII-95	1172	648

Table 1 b

List of sequences of probes informative for disease diagnosis

Please see the note at the bottom

Clone ID	Sequence ID
I-09	298
I-10	299
I-13	1331
I-14	1178
I-15	300
I-16	301
I-17	302
I-19	304
I-20	305
I-22	306
I-23	307
I-24	308
I-25	309
I-28	310
I-30	1180
I-31	311
I-32	312
I-34	313
I-37	1440
I-38	314
I-39	315
I-40	316
I-42	1332
I-44	317
I-45	318
I-46	319
I-47	320
I-48	321
I-49	322
I-53	323
I-54	1181
I-56	324
I-57	325
I-58	326
I-60	327
I-64	328
I-67	330
I-69	331
I-71	332
I-72	333
I-73	334
I-77	335
I-79	336
I-80	337

I-81	338
I-82	339
I-86	1336
I-88	1182
I-95	1337
II-02	360
II-03	361
II-05	363
II-06	364
II-07	365
II-08	366
II-09	367
II-10	368
II-11	369
II-12	370
II-13	371
II-14	372
II-15	373
II-16	374
II-17	375
II-18	376
II-20	377
II-21	378
II-22	379
II-23	380
II-24	381
II-25	382
II-26	383
II-27	384
II-28	385
II-29	386
II-30	387
II-31	388
II-32	389
II-33	390
II-34	391
II-35	392
II-37	393
II-38	394
II-39	395
II-40	396
II-41	397
II-42	398
II-43	399
II-44	400
II-46	401
II-47	402
II-48	403
II-49	404
II-50	405
II-52	406

II-53	407
II-54	408
II-55	409
II-56	410
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-63	417
II-64	418
II-65	419
II-66	420
II-67	421
II-68	422
II-69	423
II-70	424
II-71	425
II-72	426
II-73	427
II-74	428
II-75	429
II-76	430
II-77	431
II-78	432
II-79	433
II-80	434
II-81	435
II-82	436
II-83	437
II-84	438
II-85	439
II-86	440
II-87	441
II-88	442
II-89	443
II-90	444
II-91	445
II-92	446
II-93	447
II-94	448
II-95	449
II-96	450
III-01	452
III-02	453
III-03	454
III-04	455
III-05	457
III-06	458
III-07	459

III-08	460
III-09	461
III-11	462
III-12	463
III-13	464
III-14	465
III-15	466
III-16	467
III-17	468
III-18	469
III-19	470
III-20	1183
III-21	471
III-22	472
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-31	481
III-32	482
III-33	483
III-34	484
III-35	485
III-37	486
III-39	487
III-40	488
III-42	489
III-43	490
III-44	491
III-45	492
III-46	493
III-47	494
III-48	495
III-49	496
III-50	497
III-51	498
III-52	499
III-53	500
III-54	501
III-55	502
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510

III-65	511
III-66	512
III-67	513
III-69	514
III-70	515
III-71	516
III-73	517
III-74	518
III-75	519
III-77	520
III-78	521
III-79	522
III-80	523
III-81	524
III-82	1348
III-83	525
III-85	526
III-86	527
III-87	528
III-88	529
III-89	530
III-91	531
III-92	1351
III-93	532
III-94	533
III-95	534
III-96	535
IV-02	681
IV-04	682
IV-13	683
IV-14	684
IV-15	1185
IV-17	685
IV-23	1353
IV-26	1186
IV-28	686
IV-31	687
IV-32	688
IV-35	1355
IV-37	g6
IV-38	689
IV-40	690
IV-42	691
IV-43	1239
IV-44	692
IV-47	693
IV-53	61
IV-55	694
IV-56	695
IV-61	696
IV-64	697

IV-65	698
IV-69	192
IV-72	699
IV-73	700
IV-80	701
IV-82	196
IV-85	702
IV-93	703
IV-95	704
IV-96	705
IX-10	736
IX-12	738
IX-13	739
IX-24	747
IX-38	757
IX-39	758
IX-48	764
IX-50	766
IX-56	768
IX-62	773
IX-65	776
IX-72	782
IX-77	785
IX-91	796
IX-96	801
V-01	1361
V-03	706
V-04	707
V-07	708
V-08	709
V-09	710
V-11	1188
V1-16	873
V1-19	875
V-12	711
V-17	1364
V-18	712
V-20	713
V-24	714
V-25	1365
V-28	1189
V-35	1366
V-37	716
V-38	1190
V-39	1109
V-40	717
V-41	718
V-47	1368
V-48	719
V-49	1369
V-55	77

V-57	720
V-58	1370
V-61	721
V-64	722
V-65	723
V-68	1448
V-71	1495
V-74	724
V-75	1372
V-80	726
V-81	727
V-87	728
V-90	1374
VI-02	340
VI-03	341
VI-04	342
VI-06	343
VI-07	344
VI-08	345
VI-09	346
VI-11	347
VI-12	869
VI-13	870
VI-14	871
VI-16	873
VI-18	348
VI-19	349
VI-20	350
VI-21	351
VI-22	352
VI-23	878
VI-24	879
VI-25	353
VI-26	354
VI-27	355
VI-31	356
VI-32	885
VI-33	357
VI-35	358
VI-39	887
VI-43	1382
VI-44	1193
VI-45	889
VI-48	359
VI-49	892
VI-50	893
VI-53	895
VI-55	897
VI-58	899
VI-66	903
VI-67	904

VI-70	108
VI-71	1387
VI-74	905
VI-75	906
VI-76	907
VI-77	110
VI-79	1389
VI-80	908
VI-85	910
VI-87	911
VI-88	912
VI-90	1390
VI-93	1391
VI-95	915
VI-96	1392
VII-02	547
VII-03	548
VII-04	549
VII-05	550
VII-06	551
VII-07	552
VII-08	553
VII-09	554
VII-10	555
VII-11	556
VII-12	557
VII-14	558
VII-15	559
VII-17	560
VII-18	561
VII-19	562
VII-20	563
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-25	1397
VII-26	250
VII-27	568
VII-28	569
VII-29	570
VII-32	571
VII-33	572
VII-34	573
VII-35	574
VII-36	575
VII-39	576
VII-40	577
VII-41	578
VII-42	579
VII-43	580

VII-44	581
VII-45	582
VII-46	583
VII-47	1200
VII-48	584
VII-49	585
VII-50	586
VII-52	587
VII-53	588
VII-54	589
VII-55	590
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	595
VII-64	596
VII-65	597
VII-66	598
VII-67	1399
VII-71	599
VII-72	600
VII-73	601
VII-74	602
VII-76	603
VII-77	604
VII-80	605
VII-81	606
VII-82	607
VII-83	608
VII-84	609
VII-86	1453
VII-87	610
VII-89	611
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-94	616
VII-96	617
VIII-09	618
VIII-10	619
VIII-11	620
VIII-12	621
VIII-13	622
VIII-15	623
VIII-16	624
VIII-17	625
VIII-18	626
VIII-19	627
VIII-20	628

VIII-21	629
VIII-22	1455
VIII-23	630
VIII-24	631
VIII-25	632
VIII-26	1456
VIII-27	633
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	640
VIII-36	641
VIII-37	642
VIII-38	643
VIII-40	644
VIII-41	645
VIII-42	646
VIII-43	647
VIII-45	648
VIII-46	649
VIII-47	650
VIII-48	651
VIII-50	652
VIII-51	653
VIII-53	654
VIII-54	655
VIII-55	656
VIII-56	657
VIII-57	658
VIII-58	659
VIII-59	660
VIII-60	661
VIII-61	662
VIII-64	663
VIII-65	664
VIII-66	665
VIII-67	666
VIII-68	667
VIII-69	668
VIII-70	669
VIII-71	670
VIII-72	671
VIII-73	672
VIII-74	673
VIII-75	674
VIII-76	675
VIII-77	676
VIII-78	677

VIII-79	678
VIII-80	679
X-07	808
X-15	814
X-20	817
X-29	821
X-34	825
X-46	833
X-54	837
X-56	839
X-68	1207
X-72	849
X-73	1208
X-94	860
XI-13	1209
XI-37	1460
XI-43	1210
XI-67	1211
XI-81	1212
XII-07	1213
XII-35	1214
XII-36	1215
XII-59	1216
XII-65	1028
XII-92	1217
XIII-03	917
XIII-04	1218
XIII-19	1219
XIII-24	926
XIII-51	938
XIII-52	939
XIII-67	947
XIII-69	949
XIII-88	1220
XIII-92	1221
XV-22	1099
XV-24	1101
XV-25	1224
XV-42	1108
XV-62	1226
XV-64	1118
XV-84	1125
XVI-19	1228
XVI-36	1056
XVI-53	1230
XVI-60	1071
XVI-66	1074
XVI-74	1081
XVI-76	1083
XVI-77	1084
XVII-31	1139

XVII-40	1231
XVII-48	1148
XVII-76	1160
XVII-87	1165
XVII-95	1172

Note

Sequences not available for sequence IDs in Table 1, and corresponding sequence Ids in Table 2 and 4.

298,301,305,307,312,317,318,319,320,332,333,334,336,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,367,372,375,376,377,379,385,392,393,404,437,439,440,443,444,445,449,455,457,465,466,467,468,470,486,498,501,511,514,516,517,520,522,528,531,535,547,548,549,550,551,552,553,554,555,556,557,558,559,573,584,604,608,616,620,623,640,659,662,664,667,668,673,677,678,679,681,695,702,712,716,825,886,894,902,909,916,1101,1108,1109,1177,1187,1193,1204,1220,1239,1255,1256,1342,1347,1354,1357,1362,1363,1364,1373,1375,1379,1403,1404,1405,1406,1413

Table 2a

List of informative probes for diagnosis of breast cancer

Clone ID	Sequence ID
I-24	308
I-28	310
I-30	1180
I-52	-
I-54	1181
II-41	397
II-70	424
II-87	441
III-06	458
III-20	1183
III-40	488
III-57	504
III-60	-
III-61	507
III-89	530
IV-14	684
IV-15	1185
IV-26	1186
IV-32	688
IV-41	-
IV-53	61
IV-62	-
IV-69	192
IV-80	701
IV-82	196
IX-10	736
IX-12	-
IX-38	757
IX-39	758
IX-42	-
IX-48	764
IX-77	785
V-11	1188
V-32	-
V-39	-
V-55	77
V-80	726
V-94	-
VI-07	93
VI-34	-
VI-41	-
VI-48	891
VI-49	-
VI-52	-
VI-55	897
VI-65	-
VI-70	108

Clone ID	Sequence ID
VI-72	-
VI-78	-
VI-84	-
VII-03	1196
VII-15	1199
VII-32	571
VII-39	576
VII-47	1200
VII-48	1201
VII-60	-
VII-73	601
VII-77	1203
VII-90	612
VIII-20	628
VIII-29	635
VIII-30	636
VIII-31	637
VIII-39	-
VIII-44	-
VIII-46	649
VIII-48	651
VIII-66	665
VIII-74	-
VIII-76	675
X-04	-
X-07	808
X-15	814
X-29	821
X-34	-
X-35	-
X-54	837
X-56	839
X-68	1207
X-72	849
X-94	860
XI-07	-
XI-13	1209
XI-50	-
XI-58	-
XI-81	1212
XII-07	1213
XII-17	-
XII-26	-
XII-27	-
XII-31	-
XII-32	-
XII-35	1214

Clone ID	Sequence ID
XII-36	-
XII-52	-
XII-59	1216
XIII-19	1219
XIII-29	-
XIII-52	939
XIII-62	-
XIII-84	-
XIII-92	1221
XV-18	-
XV-22	1099
XV-24	-
XV-25	1224
XV-28	-
XV-34	-
XV-42	-
XV-68	-
XV-74	-
XV-93	-
XV-94	-
XV-96	-
XVI-36	1056
XVI-53	1230
XVI-59	-
XVI-66	1074
XVI-76	1083
XVI-77	1084
XVII-07	-
XVII-08	-
XVII-17	-
XVII-28	-
XVII-29	-
XVII-31	1139
XVII-36	-
XVII-39	-
XVII-40	1231
XVII-48	1148
XVII-55	-
XVII-58	-
XVII-67	-
XVII-72	-
XVII-76	1160
XVII-82	-
XVII-87	1165
XVII-95	1172

Table 2b

List of sequences of probes informative for breast cancer

Please see the note at the bottom of Table 1. Some sequences are missing.

Clone ID	Sequence ID
I-13	1331
I-14	1178
I-24	308
I-25	309
I-28	310
I-30	1180
I-37	1440
I-42	1332
I-48	321
I-54	1181
I-60	327
I-72	1335
I-81	338
I-82	339
I-86	1336
I-88	1182
I-95	1337
II-02	360
II-03	361
II-06	364
II-07	365
II-10	368
II-21	378
II-23	380
II-24	381
II-25	382
II-27	384
II-33	390
II-34	391
II-41	397
II-42	398
II-46	401
II-47	1338
II-48	403
II-52	406
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-64	418

II-67	421
II-69	423
II-70	424
II-74	428
II-80	434
II-82	436
II-84	438
II-87	441
II-88	442
II-96	450
III-01	452
III-02	453
III-06	458
III-08	460
III-12	463
III-13	464
III-17	1344
III-18	469
III-20	1183
III-21	471
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-32	482
III-33	483
III-35	485
III-39	487
III-40	488
III-42	489
III-45	492
III-46	493
III-47	494
III-48	495
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-66	512
III-67	513
III-70	515
III-74	518
III-75	519
III-78	521

III-80	523
III-81	524
III-82	1348
III-85	526
III-86	527
III-88	529
III-89	530
III-92	1351
III-93	532
III-95	534
III-96	1352
IV-04	682
IV-13	683
IV-14	684
IV-15	1185
IV-17	685
IV-23	1353
IV-26	1186
IV-31	687
IV-32	688
IV-35	1355
IV-37	g6
IV-38	689
IV-42	691
IV-43	1239
IV-47	693
IV-53	61
IV-61	696
IV-64	697
IV-69	192
IV-72	699
IV-80	701
IV-82	196
IV-85	702
IV-93	1360
IV-96	705
IX-10	736
IX-12	738
IX-13	739
IX-24	747
IX-38	757
IX-39	758
IX-48	764
IX-50	766
IX-56	768
IX-62	773
IX-65	776
IX-72	782
IX-77	785
IX-91	796
IX-96	801

V-01	1361
V-03	706
V-04	707
V-07	708
V-08	709
V-11	1188
V-12	711
V-17	1364
V-24	714
V-25	1365
V-28	1189
V-35	1366
V-38	1190
V-39	1109
V-41	718
V-47	1368
V-49	1369
V-55	77
V-57	720
V-58	1370
V-61	721
V-64	722
V-65	1371
V-68	1448
V-71	1495
V-74	724
V-75	1372
V-80	726
V-90	1374
VI-03	864
VI-04	865
VI-07	93
VI-08	867
VI-09	1378
VI-12	869
VI-13	870
VI-14	871
VI-16	873
VI-19	875
VI-20	876
VI-21	1380
VI-23	878
VI-24	879
VI-25	1192
VI-26	881
VI-32	885
VI-39	887
VI-43	1382
VI-44	1193
VI-45	889
VI-48	891

VI-49	892
VI-50	893
VI-53	895
VI-55	897
VI-58	899
VI-66	903
VI-67	904
VI-70	108
VI-71	1387
VI-74	905
VI-75	906
VI-76	907
VI-77	110
VI-79	1389
VI-80	908
VI-85	910
VI-87	911
VI-88	912
VI-90	1390
VI-93	1391
VI-95	915
VI-96	1392
VII-02	1195
VII-03	1196
VII-06	1394
VII-08	1197
VII-09	1198
VII-10	1395
VII-11	1396
VII-15	1199
VII-17	560
VII-19	562
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-25	1397
VII-26	250
VII-27	568
VII-29	570
VII-32	571
VII-33	572
VII-36	575
VII-39	576
VII-41	578
VII-42	579
VII-43	580
VII-46	583
VII-47	1200
VII-48	1201
VII-49	585

VII-54	589
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	1202
VII-64	596
VII-66	598
VII-67	1399
VII-72	600
VII-73	601
VII-77	1203
VII-80	605
VII-82	607
VII-86	1453
VII-87	610
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-96	617
VIII-09	618
VIII-10	619
VIII-13	622
VIII-16	624
VIII-20	628
VIII-21	629
VIII-22	1455
VIII-23	630
VIII-24	631
VIII-25	632
VIII-26	1456
VIII-27	633
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	1204
VIII-38	643
VIII-40	644
VIII-41	645
VIII-46	649
VIII-48	651
VIII-55	656
VIII-57	658
VIII-59	660
VIII-60	661
VIII-61	1205
VIII-64	663

VIII-66	665
VIII-73	672
VIII-74	673
VIII-76	675
VIII-80	679
X-07	808
X-15	814
X-20	817
X-29	821
X-34	825
X-46	833
X-54	837
X-56	839
X-68	1207
X-72	849
X-73	1208
X-94	860
XI-13	1209
XI-37	1460
XI-43	1210
XI-67	1211
XI-81	1212
XII-07	1213
XII-35	1214
XII-36	1215
XII-59	1216
XII-65	1028
XII-92	1217
XIII-03	917
XIII-04	1218
XIII-19	1219
XIII-24	926
XIII-51	938
XIII-52	939
XIII-67	947
XIII-69	949
XIII-88	1220
XIII-92	1221
XV-22	1099
XV-24	1101
XV-25	1224
XV-42	1108
XV-62	1226
XV-64	1118
XV-84	1125
XVI-19	1228
XVI-36	1056
XVI-53	1230
XVI-60	1071
XVI-66	1074
XVI-74	1081

XVI-76	1083
XVI-77	1084
XVII-31	1139
XVII-40	1231
XVII-48	1148
XVII-76	1160
XVII-87	1165
XVII-95	1172

Table 3

List of informative probes (Clone ID) selected for breast cancer diagnosis based on their occurrence criterion during variable selection.

Occurrence*	Clone ID
100%	XI-8,XVI-66,VIII-66,XVI-59,VII-03,XIII-19,XII-35,X-35,XI-50,XII-26,IV-53,XIII-29,XIII-62,I-30,III-06,XV-22,XV-94,VII-15,VII-39,IX-39,XVII-39,III-40,VII-32
90%	I-52,VI-65,VI-34,IV-62,XV-34,XVII-58,V-11,VI-78,XII-36,XIII-92,VIII-29,XVI-53,XVI-77,XI-13,XIII-84,IV-14,XII-31,V-80,VII-48,XVII-29,XVII-72
80%	III-60,VIII-74,IX-12,X-04,XIII-52,VIII-30,IX-38
70%	VI-49,X-29,VIII-48
60%	IV-82,IX-10,VI-52,X-68,VII-77
50%	IV-15
40%	XV-28,II-70,V-55
30%	XVII-17,XVII-67
20%	XI-58,XVI-36,VIII-39,VIII-44,III-61,IV-69,XV-68,X-72
10%	IX-42,IX-77,X-94,XV-96,XVII-55
5%	XII-59,XVI-76,I-54,XV-18,V-94,X-54,VI-07,VII-47,XVII-31,XVII-87,XVII-48
In at least one model	II-41,VI-41,III-57,III-89,VII-73,XV-25,IV-26,X-34,IV-41,VII-90,XV-42,XVII-82,XII-27,VIII-20,I-28,VII-60,VIII-76,III-20,VI-84,XI-07,XVII-28,XII-17,XVII-36,XII-52 ,XVII-76,VIII-46,VI-70,XV-74,XV-93,VIII-31,II-87,V-39 ,VI-55,X-07,X-15,XII-07,XVII-07,XVII-08,XVII-95,I-24,IV-32,V-32,VI-48,VI-72,IV-80,IX-48,X-56,XV-24,XII-32,XVII-40

*100% = Genes appearing in all the 75 cross validated models; 90% = Additional genes appearing in at least 68 out of 75 cross validated models; 5% = Additional genes appearing in at least 4 out of 75 cross validated models and so on.

Table 4a

List of informative probes for diagnosis of Alzheimer disease

Clone ID	Sequence ID
I-01	-
I-02	-
I-13	-
I-21	-
I-34	313
I-37	-
I-42	-
I-58	326
I-71	-
I-72	-
I-86	-
I-95	-
II-03	361
II-05	363
II-06	364
II-10	368
II-24	381
II-25	382
II-26	383
II-33	390
II-34	391
II-42	398
II-47	-
II-57	411
II-61	415
II-69	423
II-75	429
II-83	-
II-84	438
II-88	442
II-90	-
II-94	448
III-02	453
III-05	-
III-06	458
III-08	460
III-10	-
III-13	464
III-15	-
III-17	-
III-23	473
III-26	476
III-35	485
III-39	487
III-43	490
III-44	491
III-53	500
III-56	503
III-60	-
III-63	509
III-68	-
III-74	518
III-80	523
III-82	-
III-85	526
III-92	-
III-96	-
IV-23	-
IV-26	-
IV-29	-
IV-31	687
IV-34	-
IV-35	-
IV-45	-
IV-80	701
IV-82	-
IV-93	-
V-01	-
V-02	-
V-03	706
V-04	707
V-06	-
V-07	708
V-12	711
V-15	-
V-17	-
V-21	-
V-25	-
V-35	-
V-42	-
V-43	-
V-47	-
V-49	-
V-52	-
V-54	-
V-58	-
V-59	-
V-65	-
V-68	-
V-71	-
V-75	-
V-79	-
V-80	726
V-90	-
V-91	-
V-92	-

Clone ID	Sequence ID
VI-02	-
VI-04	865
VI-09	-
VI-10	-
VI-12	869
VI-14	871
VI-17	-
VI-20	876
VI-21	-
VI-23	878
VI-41	-
VI-42	-
VI-43	-
VI-44	-
VI-48	891
VI-49	-
VI-50	893
VI-53	895
VI-71	-
VI-74	905
VI-76	907
VI-78	-
VI-79	-
VI-87	911
VI-88	912
VI-90	-
VI-93	-
VI-95	915
VI-96	-
VII-02	-
VII-03	-
VII-06	-
VII-10	-
VII-11	-
VII-19	562
VII-21	564
VII-25	-
VII-36	575
VII-42	579
VII-43	580
VII-46	583
VII-59	593
VII-63	595
VII-66	598
VII-67	-
VII-72	600
VII-73	601
VII-75	-
VI-02	-
VI-04	866
VI-09	-
VI-10	-
VI-12	873
VI-14	875
VI-17	-

Clone ID	Sequence ID
VII-91	613
VII-93	615
VIII-01	-
VIII-02	-
VIII-03	-
VIII-06	-
VIII-09	618
VIII-10	-
VIII-15	-
VIII-22	-
VIII-26	-
VIII-28	634
VIII-30	636
VIII-32	638
VIII-33	639
VIII-41	645
VIII-42	646
VIII-48	651
VIII-58	-
VIII-64	663
VIII-65	-
VIII-67	666
VIII-78	-
VIII-82	-
VIII-83	-
VIII-85	-
VIII-87	-
VIII-91	-
VIII-92	-
VIII-93	-
VIII-95	-

Table 4b

List of sequences of probes informative for Alzheimer disease

Please see note to Table 1

Clone ID	Sequence ID
I-09	298
I-10	299
I-15	300
I-16	301
I-17	302
I-19	304
I-20	305
I-22	306
I-23	307
I-24	308
I-25	309
I-28	310
I-31	311
I-32	312
I-34	313
I-38	314
I-39	315
I-40	316
I-44	317
I-45	318
I-46	319
I-47	320
I-48	321
I-49	322
I-53	323
I-56	324
I-57	325
I-58	326
I-60	327
I-64	328
I-67	330
I-69	331
I-71	332
I-72	333
I-73	334
I-77	335
I-79	336
I-80	337
I-81	338
I-82	339
VI-02	340

VI-03	341
VI-04	342
VI-06	343
VI-07	344
VI-08	345
VI-09	346
VI-11	347
VI-18	348
VI-19	349
VI-20	350
VI-21	351
VI-22	352
VI-25	353
VI-26	354
VI-27	355
VI-31	356
VI-33	357
VI-35	358
VI-48	359
II-02	360
II-03	361
II-05	363
II-06	364
II-07	365
II-08	366
II-09	367
II-10	368
II-11	369
II-12	370
II-13	371
II-14	372
II-15	373
II-16	374
II-17	375
II-18	376
II-20	377
II-21	378
II-22	379
II-23	380
II-24	381
II-25	382
II-26	383
II-27	384
II-28	385
II-29	386
II-30	387
II-31	388
II-32	389
II-33	390
II-34	391
II-35	392

II-37	393
II-38	394
II-39	395
II-40	396
II-41	397
II-42	398
II-43	399
II-44	400
II-46	401
II-47	402
II-48	403
II-49	404
II-50	405
II-52	406
II-53	407
II-54	408
II-55	409
II-56	410
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-63	417
II-64	418
II-65	419
II-66	420
II-67	421
II-68	422
II-69	423
II-70	424
II-71	425
II-72	426
II-73	427
II-74	428
II-75	429
II-76	430
II-77	431
II-78	432
II-79	433
II-80	434
II-81	435
II-82	436
II-83	437
II-84	438
II-85	439
II-86	440
II-87	441
II-88	442
II-89	443

II-90	444
II-91	445
II-92	446
II-93	447
II-94	448
II-95	449
II-96	450
III-01	452
III-02	453
III-03	454
III-04	455
III-05	457
III-06	458
III-07	459
III-08	460
III-09	461
III-11	462
III-12	463
III-13	464
III-14	465
III-15	466
III-16	467
III-17	468
III-18	469
III-19	470
III-21	471
III-22	472
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-31	481
III-32	482
III-33	483
III-34	484
III-35	485
III-37	486
III-39	487
III-40	488
III-42	489
III-43	490
III-44	491
III-45	492
III-46	493
III-47	494
III-48	495
III-49	496
III-50	497

III-51	498
III-52	499
III-53	500
III-54	501
III-55	502
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-65	511
III-66	512
III-67	513
III-69	514
III-70	515
III-71	516
III-73	517
III-74	518
III-75	519
III-77	520
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III-86	527
III-87	528
III-88	529
III-89	530
III-91	531
III-93	532
III-94	533
III-95	534
III-96	535
VII-02	547
VII-03	548
VII-04	549
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VII-06	551
VII-07	552
VII-08	553
VII-09	554
VII-10	555
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VII-15	559

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VII-36	575
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VII-40	577
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VII-42	579
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VII-44	581
VII-45	582
VII-46	583
VII-48	584
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VII-50	586
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VII-53	588
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VII-62	594
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VII-65	597
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VII-73	601
VII-74	602
VII-76	603
VII-77	604
VII-80	605
VII-81	606
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VII-83	608
VII-84	609
VII-87	610

VII-89	611
VII-90	612
VII-91	613
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VII-93	615
VII-94	616
VII-96	617
VIII-09	618
VIII-10	619
VIII-11	620
VIII-12	621
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VIII-15	623
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VIII-17	625
VIII-18	626
VIII-19	627
VIII-20	628
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VIII-23	630
VIII-24	631
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VIII-41	645
VIII-42	646
VIII-43	647
VIII-45	648
VIII-46	649
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VIII-56	657
VIII-57	658
VIII-58	659
VIII-59	660
VIII-60	661
VIII-61	662

VIII-64	663
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VIII-66	665
VIII-67	666
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VIII-69	668
VIII-70	669
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VIII-72	671
VIII-73	672
VIII-74	673
VIII-75	674
VIII-76	675
VIII-77	676
VIII-78	677
VIII-79	678
VIII-80	679
IV-02	681
IV-04	682
IV-13	683
IV-14	684
IV-17	685
IV-28	686
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IV-32	688
IV-38	689
IV-40	690
IV-42	691
IV-44	692
IV-47	693
IV-55	694
IV-56	695
IV-61	696
IV-64	697
IV-65	698
IV-72	699
IV-73	700
IV-80	701
IV-85	702
IV-93	703
IV-95	704
IV-96	705
V-03	706
V-04	707
V-07	708
V-08	709
V-09	710
V-12	711
V-18	712
V-20	713
V-24	714

V-37	716
V-40	717
V-41	718
V-48	719
V-57	720
V-61	721
V-64	722
V-65	723
V-74	724
V-80	726
V-81	727
V-87	728
VI-13	870
VI-14	871
VI-16	873
VI-23	878
VI-24	879
VI-28	883
VI-32	885
VI-38	886
VI-39	887
VI-45	889
VI-46	890
VI-49	892
VI-50	893
VI-52	894
VI-53	895
VI-54	896
VI-55	897
VI-57	898
VI-58	899
VI-63	900
VI-65	902
VI-66	903
VI-67	904
VI-74	905
VI-75	906
VI-76	907
VI-80	908
VI-81	909
VI-85	910
VI-87	911
VI-88	912
VI-91	913
VI-94	914
VI-95	915
VI-96	916
I-13	1177
I-14	1178
I-30	1180

I-54	1181
I-88	1182
III-20	1183
IV-15	1185
IV-26	1186
IV-62	1187
V-11	1188
V-28	1189
V-38	1190
V-45	1191
VI-44	1193
VII-47	1200
I-42	1332
I-52	1333
I-86	1336
I-95	1337
III-10	1342
III-60	1347
III-82	1348
III-92	1351
IV-23	1353
IV-34	1354
IV-35	1355
IV-41	1356
IV-45	1357
IV-82	1359
V-01	1361
V-02	1362
V-06	1363
V-17	1364
V-25	1365
V-35	1366
V-42	1367
V-47	1368
V-49	1369
V-58	1370
V-75	1372
V-79	1373
V-90	1374
V-91	1375
V-94	1376
VI-10	1379
VI-41	1381
VI-43	1382
VI-71	1387
VI-72	1388
VI-79	1389
VI-90	1390
VI-93	1391
VII-25	1397
VII-60	1398

VII-67	1399
VIII-22	1403
VIII-26	1404
VIII-39	1405
VIII-44	1406
I-37	1440
V-32	1445
V-52	1447
V-68	1448
V-92	1449
VI-42	1450
VI-78	1452
VII-86	1453
VII-88	1454
IV-29	1490
V-15	1491
V-39	1492
V-54	1493
V-59	1494
V-71	1495

Table 5

Samples

Diagnosis	No. of women
Normal /Benign	42*
DCIS	3
Invasive cancer	26

* From one woman, whole blood was collected at weeks 1,2,3,4,5 following menstruation. Hence, the number of unique normal/benign samples tested in the experiment is 75

Information about women with breast cancer

Sample	*AGE*	*Stage*	*Cancer type*	*Size hist. (mm)*	*Nodes*
1	51	II	IDC	20	1/7
2	84	II	IDC	22	2/2
3	50	I	DCIS+ 1 IDC	>50 DCIS; 5 x 14	0/7
4	47	I	IDC	15	0
5	69	III	ILC g.2 + tubular adenocarcinoma	50 + 3	1 av 12 + 1 av 7
6	50	II	IDC	24	0
7	65	I	IDC	15	0
8	63	II	IDC	23	0
9	55	I	IDC + DCIS	4	0 av 1
10	52	0	DCIS + small colloid carcinoma foci	50 + 3	0
11	60	II	IDC	24	0
12	54	I	IDC	11	0
13		0	DCIS	20	0
14	49	0	DCIS	9	0
15	48	I	IDC	4	0
16	56	I	IDC	4	0
17	68	I	IDC	14	0
18	68	I	IDC	7	0
19	63	I	IDC	10	0
20	45	I	IDC	19	1
21	57	III	IDC	60	8/20
22	55	II	IDC/DCIS	35 +55	0
23	71	I	IDC/extensive DCIS	8	0
24	56	I	IDC	9	?

25	66	II	IDC	26	0
26	66	I	IDC	15	?
27	61	I	IDC	9	?
28	?	?	?	?	?
29	65	I	IDC	11	0

Other diseases /conditions present in the women tested

Other diseases /conditions present in the women tested

Disease/condition
Diabetes
Asthma
Ulcerous colitis
Hemochromatose
Crohn's disease
Fibromyalgia
Psoraiasis
Atopic eczema
Rheumatism
Allergies

Prior history of cancer in the women tested

Cancer type	No. of women
Breast	3
Colon	2
Stomach	1
Skin	1

Table 6

Number of samples tested by double cross validation and success of the diagnostic test for breast cancer based on selected informative genes

Number of samples tested by double cross validation

Number of unique samples tested	75
Number of unique non cancer samples tested	46
Number of cancer samples tested	29

Success of the diagnostic test for breast cancer based on selected informative genes

Occurrence in percentage*	Number of informative probes	Specificity	Sensitivity	Accuracy	False Positive rate	False negative rate	Total error rate
100.00	23	84.78	75.86	81.33	15.22	24.14	18.67
90.00	44	91.30	79.31	86.67	8.70	20.69	13.33
80.00	51	86.96	79.31	84.00	13.04	20.69	16.00
70.00	54	89.13	75.86	84.00	10.87	24.14	16.00
60.00	58	89.13	75.86	84.00	10.87	24.14	16.00
50.00	59	89.13	75.86	84.00	10.87	24.14	16.00
40.00	63	89.13	75.86	84.00	10.87	24.14	16.00
30.00	66	86.96	75.86	82.67	13.04	24.14	17.33
20.00	74	89.13	75.86	84.00	10.87	24.14	16.00
10.00	79	89.13	75.86	84.00	10.87	24.14	16.00
5.00	90	86.96	79.31	84.00	13.04	20.69	16.00
1.33	139	84.78	72.41	80.00	15.22	27.59	20.00

*100% = Genes appearing in all the 75 cross validated models; 90% = Genes appearing in at least 68 out of 75 cross validated models; 5% = Genes appearing in at least 4 out of 75 cross validated models; and so on.

Table 7

Double cross-validation and details of the success of the diagnostic test for Alzheimer disease based on the expression 182 informative genes

Validation Result

Total number of samples tested	14
Number of Alzheimer's disease samples tested	7
Number of Alzheimer,s disease samples incorrectly predicted	1
Number of non_Alzheimer's disease samples tested	7
Number of non-Alzheimer's disease samples incorrectly predicted	0

Success of diagnostic test

Performance	Description	%
Accuracy	Percentage of the total number of predictions that were correct	92.9
Sensitivity	Percentage of positive cases that were correctly identified	85.7
Specificity	Percentage of negatives cases that were correctly predicted	100
False positive rate	Percentage of negatives cases that were incorrectly classified as positive	0.0
False negative rate	Percentage of positives cases that were incorrectly classified as negative	14.3
Total error rate	Percentage of the total cases incorrectly predicted	7.1

Table 8

Some relevant features of the blood donors. B, Female donors with breast cancer; N, Female donors with suspected mammogram but no breast cancer; IDC, invasive ductal carcinoma; DCIS, ductal carcinoma in situ; na, not available nd, not determined; ++, no degradation of mRNA and no ribosomal contamination in the sample, +, no degradation of mRNA but ribosomal contamination in the sample.

		AGE	*Cancer type /breast abnormality*	*Size Hist. (mm)*	*mRNA Quality*
1	B1	na	IDC	5	++
2	B2	49	DCIS	8	nd
3	B3	54	IDC	18	++
4	B4	59	IDC	12	+
5	B5	61	DCIS+micro invasive cancer	15+1.5	++
6	B6	55	IDC	12+17	nd
7	B6		IDC	12+17	nd
8	N1	45	Fibroadenoma	-	nd
9	N2	52	na	-	+
10	N3	55	Cyst	-	++
11	N4	54	na	-	++
12	N5	51	Benign ductal epitelhelium	-	nd
13	N6	57	Benign	-	nd
14	N7	50	na	-	++
15	N8	52	na	-	+

Table 9

List of sequence of probes informative for both alzheimer and breast cancer disease

Clone ID	Sequence ID
I-24	308
I-25	309
I-28	310
I-48	321
I-60	327
I-72	333
I-81	338
I-82	339
II-02	360
II-03	361
II-06	364
II-07	365
II-10	368
II-21	378
II-23	380
II-24	381
II-25	382
II-27	384
II-33	390
II-34	391
II-41	397
II-42	398
II-46	401
II-47	402
II-48	403
II-52	406
II-57	411
II-58	412
II-59	413
II-60	414
II-61	415
II-62	416
II-64	418
II-67	421
II-69	423
II-70	424
II-74	428
II-80	434
II-82	436
II-84	438

II-87	441
II-88	442
II-96	450
III-01	452
III-02	453
III-06	458
III-08	460
III-12	463
III-13	464
III-17	468
III-18	469
III-21	471
III-23	473
III-24	474
III-25	475
III-26	476
III-27	477
III-28	478
III-29	479
III-32	482
III-33	483
III-35	485
III-39	487
III-40	488
III-42	489
III-45	492
III-46	493
III-47	494
III-48	495
III-56	503
III-57	504
III-58	505
III-59	506
III-61	507
III-62	508
III-63	509
III-64	510
III-66	512
III-67	513
III-70	515
III-74	518
III-75	519
III-78	521
III-80	523
III-81	524
III-85	526
III-86	527
III-88	529
III-89	530
III-93	532
III-95	534

III-96	535
IV-04	682
IV-13	683
IV-14	684
IV-17	685
IV-31	687
IV-32	688
IV-38	689
IV-42	691
IV-47	693
IV-61	696
IV-64	697
IV-72	699
IV-80	701
IV-85	702
IV-93	703
IV-96	705
V-03	706
V-04	707
V-07	708
V-08	709
V-12	711
V-24	714
V-41	718
V-57	720
V-61	721
V-64	722
V-65	723
V-74	724
V-80	726
VI-03	341
VI-04	342
VI-07	344
VI-08	345
VI-09	346
VI-12	869
VI-14	871
VI-19	349
VI-20	350
VI-21	351
VI-23	878
VI-25	353
VI-26	354
VI-48	359
VI-50	893
VI-53	895
VI-74	905
VI-76	907
VI-87	911
VI-88	912
VI-95	915

VII-02	547
VII-03	548
VII-06	551
VII-08	553
VII-09	554
VII-10	555
VII-11	556
VII-15	559
VII-17	560
VII-19	562
VII-21	564
VII-22	565
VII-23	566
VII-24	567
VII-27	568
VII-29	570
VII-32	571
VII-33	572
VII-36	575
VII-39	576
VII-41	578
VII-42	579
VII-43	580
VII-46	583
VII-48	584
VII-49	585
VII-54	589
VII-57	591
VII-58	592
VII-59	593
VII-62	594
VII-63	595
VII-64	596
VII-66	598
VII-72	600
VII-73	601
VII-77	604
VII-80	605
VII-82	607
VII-87	610
VII-90	612
VII-91	613
VII-92	614
VII-93	615
VII-96	617
VIII-09	618
VIII-10	619
VIII-13	622
VIII-16	624
VIII-20	628
VIII-21	629

VIII-23	630
VIII-24	631
VIII-25	632
VIII-28	634
VIII-29	635
VIII-30	636
VIII-31	637
VIII-32	638
VIII-33	639
VIII-34	640
VIII-38	643
VIII-40	644
VIII-41	645
VIII-46	649
VIII-48	651
VIII-55	656
VIII-57	658
VIII-59	660
VIII-60	661
VIII-61	662
VIII-64	663
VIII-66	665
VIII-73	672
VIII-74	673
VIII-76	675
VIII-80	679

Nucleotide sequences

Sequence ID - 93 nt: 405

GGATCCTGTGGCCCACAGAGCTGCCCCAGCAGACGCTCCGCCCCACCCGGTGATGG
AGCCCCGGGGGGACAATCGTGCCTGGGGAGGAGCAGGGTACAGCCCATTCCCCCAG
CCCTGGCTGACCTGGCCTAGCAGTTTGGCCCTGCTGGCCTTAGCAGGGAGACAGGG
GAGCAAAGAACGCCAAGCCGGAGGCCCGAGGCCAGCCGGCCTCTCGAGAGCCAGAG
CAGCAGTTGAATGTAATGCTGGGGACAGGCATGCTGCCGCCAGTAGGGCGGGGACC
CGGACAGCCAGGTGACTACCAGTCCTGGGGACACACTCACCATAAACACATCCCCA
GGCAGGACAGATCGGGGAAGGGGTGTGTACCAGGCTATGATTTCTCTTGCATTAAA
ATGTATTATTATT

Sequence ID - 108 nt: 550

GGCTTTGACAGAGTGCAAGACGATGACTTGCAAAATGTCGCATCTGGAACGCAACA
TAGANACCATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGAC
ACCCTGAACCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCT
CAAGAAGGAGAATAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACA
CAAATGCAGACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTA
ACCTGGGCCTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCA
TAAGCCAGGCCTCGGGGAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTG
GCCACGGCCACGGCCACAGTCATGGTGGCCACGGCCACAGCCACTAATCAGGAGGC
CAGGCCACCCTGCCTNTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAACTGTC
TTGGCTGTGGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCTCC

Sequence ID 110

ACGAAGACAGACATCTGTGGAATGATTCACATCCTCTCAAGTTAGGAGGATGGAGG
CCTGCTTCATTAAGAAGCTGGGGGTAGGGTGGGGGTGGGGAGAACACTTAACAACA
TGGGGACCAGTCAGGGGAATCCCCTTATTTCTGTTTTGCATATGAGGAACCCTAGA
GCAGCCAGGTGAGGCTCTCTAGTTTAATAAAAATCATGGAAAGACTCTTAATGCAG
ACTCTTCTTAAGTGTTAATAGGGATTTTTTCAGCTTATTTGGTTGCAGTTTCCAA
TTTTTAAAAATGTTGAGGTAATCTTTCCCACCTTCCCAAACCTAATTCTTGTAGAT
GCATTAGTGTTGAACCAATGCTTTCTCATGTCTCAATTCTTTGTATATGCATTCTT
TTCAGATGTATTAAACAAACAAAAACCCTTC

Sequence ID - 192 nt: 286

CCGGTAATAGAATAGAAAAGGGAGAGTGTCTTCATGCAATGTGGCATCCTGGATTG
GGTCTCGNNACAAAAACAGGACATTAGTGGGAAAATTGGAAATCTGAAAAAAGTCT

GAATTTTAGTTAATATACCAATTTCAGTCTCTTGGTTTTGACAGATGTACCATGGT
GATGTAAGATGTTGACCTTGGGGTAGGCTGGGTGAAGGGTATACAGGAACTCTTTG
TACTATCTCTGCAACTTCTCTGTAAATCTAGTATCATTCCAAAATAAAAGTTTATT
TAATTT

Sequence ID 250

GTGGAAGTGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGA
TGCCCAGGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAA
CTATTGGATGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAA
GCAGATGCAGCAGATCCGCATGTCCCTTCGCGGGAAGGCTGTGGTGCTGATGGGCA
AGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTG
GAGAAACTGCTGCCTCATATCCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGA
CCTCACTGAGATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTG
CTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGG
CCCGAGAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCACTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCACTGATCAAGACTGG

Sequence ID 299

CAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAG
TTTTTTTCTCTTTGAAAGATAGAGATTGNTACAACTACTTAAAAAATATAGTCAAT
AGGTTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAG
ATTTTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAA
AGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATG
TATTTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGA
AGGGCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTT
AAAAGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAAC
CGAAGGTGATTAAAAGACCTTGAAATCCATGACGCANGGAGAATTGCGCATTTAAA
GCCTAGTTACGCATTTACTAAACGCAGACGAAAATGGGAAGATTAATTGGGAGTGG
TAGGATGAAACAATTTTGGAGAAGATAGAAG

Sequence ID 300

CTCAAAGGAGAAAAAAAACCTTGTAAAAAAAGCAAAAATGACAACAGAAAAACAAT
CTTATTCCGAGCATTCCAGTAACTTTTTTGTGTATGTACTTAGCTGTACTATAAGT
AGTTGGTTTGTATGAGATGGTTAAAAAGGCCAAAGATAAAAGGTTTCTTTTTTTTT
CCTTTTTTGTCTATGAAGTTGCTGTTTATTTTTTTTGGCCTGTTTGATGTATGTGT
GAAACAATGTTGTCCAACAATAAACAGGAATTTTATTTTGCTGAGTTGTTCTAAAA
AAAAAAAAAAAAAAAA

Sequence ID 302
AGTAGAGACGGGGTTTCACTGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGT
GATCCGGCCACCTCGGCCTCCCGAAAGTGCTGGGATTACAGGCGTGAGCCACGGCG
CCCAGCCCCAGCCTGTCACTTAAACTGATAAACGACAGATTAACAGTAGAAAAATT
TTATTTTGCATACATAATGAGGCTTCACAAAAGAGAAGTGAAAACCCAAGTAGGAG
TTTAGGGCTGGGGGCTTATATACCATTTAACAAGGGGTGATAAATTGTAAGAGAAT
AG

Sequence ID 304
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ATATGTAACAGGTGCCATTGTTACTGTAACTTTTCACACATGCCTTCAGTTTGATG
TCAAAGTCATCATTTAGTGTAAACAGCAAGTTATCTGTTAGGCTGCACATCATGAA
CTTTACTTTTAGAAAGTCTTATCTTTTATGCCACAGAAATAGCATTTGGCTATTAG
TCATGGATGGCAAAGAAATTAATTTTGAGTTGTTTGGATAAAAATGTTTCAGTTGA
CTGTAGTGTGTATTGAGAGACACTGCCAGTAAACAAACTCTCTTGGTAGGTGGAAA
TCCCCTAGAAGTTACAGAAAATTGGGAGGAGGTGAACTTAATTAAATAACTTGAAT
TGTTTAGACATATTCAGAGCTTCTTATGACCTTGAAGAAATCACCCAACTTCAAAA
GACCTCGGTTTCTTCATTTGTAAAATTAGGGAGTTTGACTAGATGTGTAAATCTAG
TTGTTAGTTAACTTCTAAGATGTAAAAACCCTCTTGTTTAACAAAAACCTACAAGA
TCAAGTTGCTTATCTGAAATCTTTATGAATCAACACTAGTCACTAAGTCTAGCTCG
ACC

Sequence ID 306
CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTC
TGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTC
GACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTC
CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
CAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTT
CCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCAT
CAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACAA
TGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATAC
CAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGTG
AAGGATGCNCATGAANAAATGGACNAGCTGTG

Sequence ID - 308 nt: 373
AAGTGGGTCTTGCCATCCCTGAACTGNAATCATCCCTAACATATTCATACCTGTTT
TCATTTTAAAAGTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGA

TTTATTTGCTATATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGT
CCTGTATGGAGACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTG
AATATTGGTGNATAAATCCATACNCACCACGTACATATCTTAAGTTCTGGAAGAGA
TATTGCTAAACCAGAAGATAACCTGCATTTAAAATTTGACTGCTAGGGNCAGGGNC
ACATTTAATTAAATTAGAACAANGAATGCATAATGNC

Sequence ID 309

CCGGAATCGCGGCCGCGTCGACGAAAATATGTGCCCTGGCCAACTCCACAGGACTA
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TATACTGAAGTAGTATTTAATATTCAAGTACTTGTAAATTTGCAGAACAGTACTTT
TTAATTTGACCCATGAATTCTATTTAAATTTGTCACTTAATATTTAGCCAAGAAGC
AAACCATCTAAAAAGATTTCTGGTTTATTTCTCCAACTCCTAATAAATAGGGTCAC
ATATTTTTTAACTTTTTTCTAATTTGAAAAGTAATACAGGCATATGGTATTTTAAA
AATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTCTTGCCATCCCTGAACTG
TAATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAAGTTGGGTCAGTTTTT
TTATTAGTACATGTATTTCTATCCTACTGATTTATTTGCTATATCATCTAATTTAG
TTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAGACCTAGCTCTTCTCA
GTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGNATAAATCCTACACAC
CACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAAACCAGAAGATAACCTG
CATTTAAAATTTGACTGCTAGGGTCAGGGTCACATTTAAATTAAATTAGAACAAGG
AATGCATAATGTCTTCGATAGCAATCTATTCAAGGTGCACCGTGGTCACAAAGGAA
AGCAAAACTGTC

Sequence ID - 310 nt:564

CCTGGNCAGAGGCCTCTATCCTGTANTGATAATTGCCATCAAAATTGTCAAAAANG
ATTTAATTTCTATGGGNAATAGTCCTTTTCTTAGCTTCTGCCNNTCACTTGCTTAT
TTTTTGTGTGGGAATGGGGTTGGATAAACCAATGAACTTTATTATAAACAAATCCC
ACCTATATCTANCAAATTTATATTTTCGGTGAAATACAGATATTTGCCTTTCTGGA
GTANTATAGAAGCTGTCAATATGTATCTACTGTACAGTACTAAATAGTATTCATTT
ATGAAATGAGTAGTGTTTGGGTGGCTGGGGTTAAGGAAAAATGAGACTTGGAATTG
TAGCTTTTATCCAAGTTTTGAGTATAAATAGGGTTTTGTTTTGTTTTTTTTAACCT
AAAAACTGAAATGCCATATAGAAAAACAGCATTGTTTTTACAGTTTGTAGTAAGTA
ACTTTTTAAAGATTTTATCAAAAAGAATTTTGTCTATNGTGAGTAAAAGAAGTTCT
AATAATGGCCTAATCACTGCATTTTTAAAAAACAAAGTTCAACACAAATGACATTT
GTTT

Sequence ID 311

CCTCTCCTCCATCTAAAGGCAACATTCCTTACCCATTAGTCTCAGAAATTGTCTTA
AGCAACAGCCCCAAATGCTGGCTGCCCCGGCCAAGCATTGGGGCCGCCATCCTGC
CTGGCACTGGCTGATGGGCACCTCTGTTGGTTCCATCAGCCAGAGCTCTGCCAAAG
GCCCCGCAGTCCCTCTCCCAGGAGGACCCTAGAGGCAATTAAATGATGTCCTGTTC
CATTGG

Sequence ID - 313 nt: 554
CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAG
GAACTTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTT
ATAGATTAAAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGAT
ATGGATTANAAATCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAAT
ATGGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTT
AATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAA
TATGGGTTAAAAATCAAAAGAAAATGAACTATTTGCTCCAGTGCAGGAAAATACAG
GCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTTGA
AGAAGAGAATAAGGNGCTAGCATTCCTATCCGTAGATAATTTGACAGCTAGGAAAT
AGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGC

Sequence ID 314
CTTTTCCTCCCGCTGTCCCCCACGGAGGGGACTGCTCTCCCCCGCTGCATCCTTTC
TGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCTC
GACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGTC
CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
CAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCTT
CCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCAT
CAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACAA
TGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATAC
CAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGTG
AAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAAGAATGTGACCCTTACTCTGG
CCTCTTGAATGATACTGAGGAGAACAACTCTGACAACCACAATCATGAGG

Sequence ID 315
TGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAGCCAAACCAGCAGC
CCCTCAGCATCCAGCAGCATGAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAATGC
CATAATCCACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTG
CCCCCTGAAACAGCTGCCACCATCACTCGCAAGAGAATCCCCTCCATCTTTGGGAG
GGGTTGATGCCAGACATCACCAGGTTGTAGAAGTTGACAGGCAGTGCCATGGGGGC

AACAGCCAAAATAGGGGGGTAATGATGTACGGGCCAAGCACTGCCCAGCTGGGGGT
CAATAAAGTTACCCTTGTACTTG

Sequence ID 316

CGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATACTAAT
CTCCCTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAA
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Sequence ID 321

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TATGGTATTTTAAAAATGAAACAACACAAAGGGATATGTTTTGAAAAGTGGTTCTT
GCCATCCCTGAACTGTAATCATCCCTAACATATTCATACCTGTTTTCATTTTAAAA
GTTGGGTCAGTTTTTTTATTAGTACATGTATTTCTATCCTACTGATTTATTTGCTA
TATCATCTAATTTAGTTTGAATATTCCATAATTTACTTAATTAGTCCTGTATGGAG
ACCTAGCTCTTCTCAGTGTCTACTATTATAAACAATGCTACAGTGAATATTGGTGT
ATAAATCCATACACACCACGTAACATATCTTAAGTTCCTGGAAGAGATATTGCTAA
ACCAGAAGATAACCTGCATTTAAAATTTTGACTGCTAGGGTCAGGGTCACATTTAA
ATTAAATTAGAACAAGGAATGCATAATGTCTTCGATAGCAATCTATTCCAGGTGCA
CCGTGGTCACAAAGGAAAGCAAAACTGTCAATAACTTTCTTCTCA

Sequence ID 322

TAGCATTTGGCCTTTTAAAACATTTGTTTATTTTTTTTCTGAGAATGGCTAACACA
CTTTATTGAGGTTCGAAATTAATAAAGAAAATAAAAGAAATGTATCTTCATTCATT
CTGTATGTTAGTGTTTTAATTACCCTTAGAATATATGGATAAAAAATACTATTCTT
TGTCTTGGAGAAGGTAAGAGTCTAGTTAGATGAATAAGGGTTATCTATGTAGAACA
ACTAGAGAATGAGAAGAGAGCTTATGAGATTGAGTACTACGTTATGCAGTAGAGTA
GCACGTCATCTGCTACTGAGTATGGTGTGATAACATTGTGTAACAGGAAAGTATGA
TCAATATCTACTTAAAATTAAGGACAATATTAGCACTACATTGCTTTATTTTAAAG
TAAAAATTAGAGAACTAAACACAAGCATTGTAAGTACAATAAAAGCTGATCTTTCT
AGTTAAGCAGAATAATACATGTTCAAGCATCTGCTAAATCATTAAATATAAGAATA
TAGGGGTTTTCTATAATCTTATTTTCTTTGGAAGAGTACCTCATTTTCAAGANGAG
AAGTTTCTAATTGCCACTTCTTTAAAAATAAAACAGGGTTTTAATGTTCCCAGCAC
AAAAATTAATATCTCTTCAAAAAGTCTCTTGTGATTAAGTTTGAATCCCTTGTCAT
ACTGCTTCTAATATTGACACTGACCTCCTTAGGTATTTTTCAGGGGTTATAATCTT
TTCTTAAGGTATCTTTTTTCAAGAATTGGATACCTTGGGCTT

Sequence ID 323

CGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGA
AAGAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAG
CTAGTACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAG
AATAAAAGGAATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCC
TCAGCCTTTGGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTT
TGGTTAGAAGAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGT
TAAAAAAAGATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTTTT
CTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAATG
CATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGTTGAGCT
GATATGGAAAAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGCTATCCCACCCC
AAATTCAACCTGAGGTATATTTCAGTGAAGCAGGTAGCTGTGCTTCTCAAAGCAGA
GAAGCAGTTTTAAGAACCAAAAAGGTAGAGGAAATCTA

Sequence ID 324

GTTTGTTACAGGCAGAATTGGATAGATACAGCCCTACAAATGTATATGCCCTCCCC
TGAAAAAAATTGGATGAAAATCTGCACAGCAAAGTGAAACACACAGATAATAGGAA
CAAAATGTAGTTCCCATGTGCCAAACAAAATAAATGAAATCTCTGCATGTTTGCAG
CATATCTGCCTTTTGGGAATGTAATCAAGGNATAATCTTTGGCTAGTGTTATGTGC
CTGTATTTTTTTAAAATGGTACACCAGAAAAGGACTGGCAGTCTACTTCTACCATA
GTTAAACTTCACCCTCTTTAATTTCACAACATATTCTTTGGAAGCAGGAAGAAATG
CTCATAAAGAGGATCAGACCTTCTTTCCCGTGAAACCAGTATTTGGCGCCATATAT
AAGCCTGGTTAAATTGGTCATCTAAAGCTGTCAAATAAGACATTCTGTGAAAGGTA
AACATCGAAACTGGTTATAAGTAAAACCATCAAGCCAACAACAGGGTCTTGAGATA
ACCTTTGAAGCTTATTGTCTGGCCTGCACCAGAAGATGTCTGCATTACTCATTGCT
AAAAATGTGTACACAGAACTGCACTAGGATTAATTGGTTCAAGAAGAAATTTAAAC
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GCAA

Sequence ID 325

GACCAGTAATGGCTTTTAAGAGTCCATTTTGTCATTGTCTCCCTAGTTAATTACAG
GTGGGGGATCTTTTGCCTCTATTCTCTTCATATTGAAATGAATCATACTCATGTTT
TGTGGAACTCCTTAAAGTTGTAGCTGTCATGATCAGATTTTTTTATATTTCCTCA
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AGTGACACATAATCTTATCTCTTTATAGAACCTTAAATTTTATCATTATTTTCGCT
TAGAATACAGCATTTCTTTGCTTCTGTTGCTGGTTTGACTTAAGAAATAAGGCAGT
AACTCTGATCAATCAATTATCCATAAGGAAGGGCTTTTCATGGGTTCTATTAATTT

GTTAGTACCCTAAGTATATCTGAAAAATATGTCTATTGAGAGAAGATTTTGGCATT
CCAGATGGTATAGTCTATATATATTTAAAGTTTTGAATTTGCTTATATATACTCAG
CTTTCTTTTTCTAGCATTTTTGCATTTACCTGTTAATTGAAGTATACCCCCCACAT
ATAAAAGTTCCTCTTAAAGACACTGGACTCTTTCTGGGGGGCTAAAATA

Sequence ID - 326 nt: 554
CCCGGAATCGCGGCCCGCGTCGACAACAAACCTGCATGTTCTGCACATGTATCCAG
GAACTTAAAAAAAAAAAAAGATAGTTTGTGTGTCTTAATTGAATAATAGTAGATTT
ATAGATTAAAGATCTATGGGTTTTTAATATGGATTANAAATCTGTGGGTTTTTGAT
ATGGATTANAAATCTGTGGGTTTTTAATATGGATTGGAAATCTGTGGGTTTTTAAT
ATGGATTAAAAAACATCTGTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTT
AATATGGATTAAACATCTGGGTTTTTAATATGGATTAAACATCTGTGGGTTTTTAA
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GCAATACTGGATACAATTAGATGGTCAGGAGCGATAACCCGGTTGCCATTGTTTGA
AGAAGAGAATAAGGNGCTAGCATTCCTATCCGTAGATAATTTGACAGCTAGGAAAT
AGGGGGAGTCTTCTATGTAGTTAGTGAAGGCTAAATGAACTATTATATGC

Sequence ID 327
CGGCTACCGACAGAAGGACTATTTCATCGCCACCCAGGGGCCACTGGCACACACGG
TTGAGGACTTCTGGAGGATGATCTGGGAGGGGAAGTCCCACACTATCGTGATGCTG
ACGGAGGTGCAGGAGAGAGAGCAGGATAAATGCTACCAGTATTGGCCAACCGAGGG
CTCAGTTACTCATGGAGAAATAACGATTGAGATAAAGAATGATACCCTTTCAGAAG
CCATCAGTATACGAGACTTTCTGGTCACTCTCAATCAGCCCCAGGCCCGCCAGGAG
GAGCAGGTCCGAGTAGTGCGCCAGTTTCACTTCCACGGCTGGCCTGAGATCGGGAT
TCCCGCCGAGGGCAAAGGCATGATTGACCTCATCGCAGCCGTGCAGAAGCANCAGC
AGCAGACAGGCAACCACCCCATCACCGTGCACTGCAGTGCCGGAGCTGGGCGAACA
GGTACATTCATAGCCCTCAGCAACATTTTGGAGCGAGTAAAAGCCGAGGGACTTTT
ANATGTATTTCAAGCTGTGAAGAGTTTACGACTTCAGAGACCACATATGGTGCAAC
CCTGGAACAGTATGAAATGTGCTACAAAGTGGTACAAGATTTATTGATATATTTCT
GATTATGCTAATTTCAATGAAGATCCTGCCTTAAATATTTTTTAATTTAATGGCAN
AT

Sequence ID 328
CAAGACTCCATCTCAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTAT
TAACACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAA
CAGGTAATTTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATT
TTAAATGTTAATGTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTG

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ACAATTACTGGTGTTTAACTGCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAA
TATTTAGTCCTTCTGAGATGGCTTGAATATTTGAATTTTGTTGTACGTCTATACTG
GGTAGTCACAAGTCTTATAAACACTTTAGAGGAAAGATGGATTTCAGTCTGTATTT
TTAAACATCATTTATTTTAAATCTGGTGCTGAAAAATAAGAAAAAAATTAAACTGC
ATTCTGCTGTTCTTCTTTANAAGCATTCCTGCGTAAATACTGCTGTAATACTGTCA
TGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCAGTGGTTTTT

Sequence ID 330
GCGGGAATCGCGGCCCGCGTCGACCTCAAAGGAGAAAAAAAACCTTGTAAAAAAAG
CAAAAATGACAACAGAAAAACAATCTTATTCCGAGCATTCCAGTAACTTTTTTGTG
TATGTACTTAGCTGTACTATAAGTAGTTGGTTTGTATGAGATGGTTAAAAAGGCCA
AAGATAAAAGGTTTCTTTTTTTTTCCTTTTTTGTCTATGAAGTTGCTGTTTATTTT
TTTTGGCCTGTTTGATGTATGTGTGAAACAATGTTGTCCAACAATAAACAGGAATT
TTATTTTGCTGAGTTGTTCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAATTTTAAAATTTTTAAAATAAAACCCTTGGTTAT

Sequence ID 331
GCCGCGTCGACCTGCATGAGCCACAGTTTCTTGACTGGAGGCCATCAACCCTCTTG
GTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGGCACTGGTGGGCCTGGGCTT
CTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCCGCTTTCCTGGGCCTCTCAG
TTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGAAAGATTANAAGCCTGGAAT
AATCAGGCTTTTTAAATGATGTAATTCCCACTGTAATAGCATAGGGATTTTGGAAG
CAGCTGCTGGTGGCTTGGGACATCANTGGGGCCAAGGGTTCTCTGTCCCTGGTTCA
ACTGTGATTTGGCTTTCCCGTGTCTTTCCTGGTGATGCCTTGTTTGGGGTTCTGTG
GGTTTGGGTGGGAAGAGGGCCATCTGCCTGAATGTAACCTGCTAGCTCTCCGAAGC
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CGTGTTGCCTACATGTCCCTGGCTTGTTGAGGCGCTGCTTCAACCTGCACCCCTCC
TTGTCTCATAGATGCTCCTTTTGACCTTTTCAAAATTAATATGGATGGGAAAGCTC
CTATGCCTTTTGGCTTCCTGGTAGAAGGCGGGATGCCCAAGGGTCTGCCTGGGTGT
GGATTGGATGCTTGGGGTGTGGGGGTTGGAAACTGTCTTGTGGCCCACTTGGGCCC
C

Sequence ID 335
CCCGCGTCGACTTTTAAAGTCATCTCTATAGGAAGGTGCTGGCAGGGATCCCAGA
GAAAGAAAGGGTCCAAGACTCCATTAACTGCCCTGGATGAAGGCACTGCTACAGC
AGCTAGTACCAGAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAG

AGAATAAAAGGAATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAG
CCTCAGCCTTTGGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAG
TTTGGTTAGAAGAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATT
GTTAAAAAAAGATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTT
TTCTTTCCAATGGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAA
TGCATCATCAGTCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGGTGAG
CTGATTTGGAAAACTGCCCTTCTGCAAAAAACACTGGCCTGCTTTCCA

Sequence ID 337
CAAGACTCCATCTCAAAAAAAAAAAAAAAATCTACAGTGCTGAGTATATAAAATTAT
TAACACATTTCACAACAATATGTGTTTGTGGAGTTAAATATTTTTTGTCTTTAAAA
CAGGTAATTTTAGTGCATACTTAATTTGATGATTAAATATGGTAGAATTAAGCATT
TTAAATGTTAATGTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTG
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ACAATTACTGGTGTTTAACTGCCAAATATGGGTAAATAAGGGAAAATTTTGTTTAA
TATTTAGTCCTTCTGAGATGGCTTGAATATTTGAATTTTGTTGTACGTCTATACTG
GGTAGTCACAAGTCTTATAAACACTTTAGAGGAAAGATGGATTTCAGTCTGTATTT
TTAAACATCATTTATTTTAAATCTGGTGCTGAAAAATAAGAAAAAAATTAAACTGC
ATTCTGCTGTTCTTCTTTAGAAGCATTCCTGCGTAAATACTGCTGTAATACTGTCA
TGCAAAGTGTATCCTTTCTTGTCGTATCCTTTTTGGGGCAGTGGTT

Sequence ID 338
CTGGACTGCATGACCAGATCTGATGGGTGAGACTCAGGTGGCATGGAAGAGCCGAA
AGAGGATACCATATGTGGGTGCCGGGGGGGATAGGTGAGAAGTACTAGAAGGCGGA
ATGGAAGGACACTTCTGCTCAGCTCTGTGACACGGGCAGGGACCCTGCAGGGCTCA
GGTCCTTTAACACAGCAGCTTCATTCTAACACCAGCAGCGTTGGAACACACGTACA
AGTATGCAGACTAAGCTCTTGCTTGGCTGATACGGCTTTTTGGGTTTTTAGAGAAC
ATGCATATATGTTCTCATTCATGGTACATGAACTCAGAAGCCTTACTGCCTATTTT
TGTTAATACTTCTGGGCAAACATTACCACTTACAACTCACACCAGTTAGAAATCAT
TTGTAAAATGTTATTTAATAAAGCCAAAGAACTAAATCATATTTATTTTCCAAGGN
TTTCTAAGATCTCTGAAACTAATGAGGTTTTTTAAATCCCCATTAAGTACTCATCA
CTGCTAGTAAAAGCAGTTGTCTTTACCTTTAATTCCAGTGAGTCCCCTTAAATTTA
TTTTTTATTATCTTTGGCTACATTGCCTTAGACAAAATGTGGTCACCCTAATTTAA
NGGATAAAATTCACATCCTCACAGATTTCTTATTAAGAGGGTCTAANCCTTGAATA
ATCANCAGTGGAAATGGAAGTCTTCTTTACTGGNTTTNATCCTTTCCCTTTTTTAT
CCCATG

Sequence ID 339
TTTTTTTTTAAATAAAGCTGTCGGCACTCAAGGGTAATTTCATATCAGTGTGNTCT
ACAAGCTGGGGGAAAATGAGTTCTAATTGTCANAGCTACCAAATCCTTCACCTTTA
GCATAAAGGTTTAAAGATATCACAAAGATGCCAAGTGATTAATAATGTTTTAAACC
ACCCCTTTTTCTGTCTGAAAAAACAACTAAAACAATATTACAACAGTATAGTTACA
GAAGGGTTCTATTTTCATATGTTTTATGCACACTGTGCCTCAAAGGTACTATTTAA
ATATATATACTTTTGAGGGGGTGGCTAATGCAGAAACACCCAAGACCTAAGGAAGA
TACAACCCCATTTCTAGGTGTGAGGTCTAAATGCTTCACACACCCACTTGTGACCT
TTTTTCATGAAGAATCATAACACTGTGCAGTGAGAAACAGTGGCAAAGCAATACTG
AAAGCATTTTAAATTATTTACTAGGTTAAAAGGGTGAACTGATACTTTAAATACAT
CAAATTTCATCAT

Sequence ID 360
GCAAGTGAGAGCCGGACGGGCACTGGGCGACTCTGTGCCTCGCTGAGGAAAAATAA
CTAAACATGGGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGC
ATTTTTTGTGCAAACTTGTCGGGAGGAGCATAAGAAGAAGCACCCAGATGCTTCAG
TCAACTTCTCAGAGTTTTCTAAGAAGTGCTCAGAGAGGTGGAAGACCATGTCTGCT
AAAGAGAAAGGAAAATTTGAAGATATGGCAAAAGCGGACAAGGCCCGTTATGAAAG
AGAAATGAAAACCTATATCCCTCCCAAAGGGGAGACAAAAAAGAAGTTCAAGGATC
CCAATGCACCCAAGAGGCCTCCTTCGGCCTTCTTCCTCTTCTGCTCTGAGTATCGC
CCAAAAATCAAAGGAGAACATCCTGGCCTGTCCATTGGTGATGTTGCGAAGAAACT
GGGAGAGATGTGGAATAACACTGCTGCAGATGACAAGCAGCCTTATGAAAAGAAGG
CTGCGAAGCTGAAGGAAAAATACGAAAAGGTA

Sequence ID - 361 nt: 622
CTGTNATNGAATCTGCTTGTNACTNAAATGCTAAACTCAATTCTGTAATTCAATAG
GTGCACCTNTCTGAGAAACATANNAGACAATGAGGAAAAGGATTCANCATTCCGTG
GAATTTGTACCATGATCAGTGTGAATCCCANTGGCGTAATCCAAGTAAGATGTTCA
CAAAGATTTGTTTTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAA
TACTTTAATTATAAAAAGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCT
TTAAAATGTATATTTCTTAATATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAA
TTTTTTTTGTCATGAAATGAGATAGTAACAGCAGATTGGGACAACAAGGTTATATT
CTTGTCTTGAATCAGGCCATGGCTTCTTTCATCCAAATTTCAGACCTCATTTATTT
ACTTTGTCCCTGCCTCCCATCCCTGGATATCANGTTTGTGGATATCTACAGTTAAT
AGAGTGACCAAATAGTAGGAATACTGTCTCTCTATTCTGAATAAAATACTTTGAAT
CAGATTTAGAAATAATGAATAAAATACAAATCACCATTGAAATTGCTCTAATTTTG
AGAGCT

Sequence ID - 363 nt: 628

ATCACNTGAGGCAAGAGTTTGAGCCAGCCTAGCTAACATGGTGAAACCCCATCTCT
ACAAAAATATAAAAATTAGCCTGGGTGGTGATGGGCACCTGTAACCCCAGCTACTC
GGGAGGCTGAGGTAGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCC
AAGATCGTGCCACTGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAA
AAAATAATAATAATAATAATAATAAAAAGGAATAACATAGCTAGGAATAAATTTAA
TCAAAGAGGTGAAAGACTTATACACTTAAAACTACAAAAAAAAAATCACTGAAGGA
ATTATAGACCCAAATAAAAATAAATAAAAAGACATTCTGTGTTTTAGGGAAAGAAG
ACTTAATATTGTTAAGATGTCAATACTACCCAAAGTGATCTACAGATTCAACATAA
TCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAATGGAAAAGCCAATTTTCAAA
TTCAGATGGAATTGCGAGGGGTTCTGAATAACAAAAACAATCTTGGGGAAAAAAAA
CAAAAAACAAAGTCAAAGAACTCACACTTCTCTATTTATAAATTTACTACAAAGTT
ATAGTAATCAAA

Sequence ID - 364 nt: 528

TGAACATCCAGCCATGTCATTTCTTCCATTCCTGCCCTGGAGTAAAGTAGATTTAC
TGAGCTGATGACTTGTGTGCATTTGTACATTGCAACCTTAGCTTACCTCTTGAAGC
ATGTAGAGCATTCATCACCCACCATTCATTCACTGCCTACTCCCACCACAGCTGTT
TCGTGGTCTGTCTGCTCCCTGTGCCACCCCCACCCCATCAGGTGGGCCTTTTGCAA
GTGATGAAGTCACCTGTGGGGGAAGAGCTTTCCTTTCCTCTCCTCAACTCAGAAGG
CCTCTTCCTCTTGCTCAAGAGGGTGCTGCTGCTTTCTGCCTCCTTCCCCGGCCGGC
CTCCATCCCAGTTCACCTTTTCAGAAATGGCCCCTCAGTCAACTCTTCCCTTTTCT
CCTGGCTTTTTATTTCTCCCAGTCTCTTAAGAGTATCCTTAGCTTTAAAAACAATA
ACACAGAGGATGGGTGCAGTGGCTCATGCCTGTAATCCCAGCACTTTGGAGCCTGG
GGCGGGCGGATCACTTGAGGNCA

Sequence ID 365

GTCCCGGAATCGCGGCCGCGTCGACCTTTTCTATGCCTGCTATATAAACAGTACCT
TGCAAGATGTCCTGTCTGATATCCACAAAGGGGTATTGTCAACCCCAAGTTCAGAC
AGCTTTGTATTCTTCTGTCCCTGGATACATGAATTACTGCCATCTTTACACAGCGC
CCTAAAATACCAACGCGAAGTTACCTGCTCAGCTTGAAGCTGCGCTGTACCCTGGA
ACCAGCACTTCTGCTGAATGACTCAGGATGAAGCCTCGACTTCTCCTTCCCATCCC
ATGCCCAGACCCCAGTGGCTCCTTTCCCAATCTGATCCAGTGACTTTAAGTCCAGC
TGTTGCAACCTGGGCATGAGGAGGAGTGCAAGATGGCTTTGTCCTACCTGGAAAGA
GGCTTTCTGGA

Sequence ID 366

CACCATTTACACACAGTGGGTCCTTGAATAGCATCGTTTTATTCAATGTCATTTTG
TTATAACATTGAGAAAAAAATTGATTCCCGGCTGGGGCCACTGTCTGTGCACCGT

Sequence ID - 368 nt: 329
GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGA
GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAG
AAGCATCAAATAGACTCAATAAAAAATGATAAAGGGGATATCACCACCAATCCCAC
AGAAATACAAACTACCATCAGAGAACACTATAAACACCTCTATGCAAAT

Sequence ID 369
GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGA
GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACAGAATTGACAGACTGCTAGCAAGACTAATAAAGAAGAGAG
AAGCATCAAATAGACTCAATAAAAAATGATAAAGGGGATATCACCACCAATCCCAC
AGAAATACAAACTACCATCAGAGAACACTATAAACACCTCTATGCAAATAAACTAG
AAAAT

Sequence ID 370
GAAAGATCTAAAATCGACACCCTAACATCACAATTAAAAGAACTAGAGAAGCAAGA
GCAAATTCAAAAGCTAGCAGAAGGCAAGAAATAACTAAGATCAGAGCAGAGCTGAA
AGAGATAGAGACACAAAAAACCATTCAAAAAAAAACAATGAATCCAGGAGTTTTTT
TTTTAAAAAGATCAACA

Sequence ID 371
GCCCGGAATCGCGGCCGCGTCGACGTAAGCTCGGCTGAATCCACGGTTCAAGAACA
GGAAAGAAGGCCAAGGCATAGGGAGTGGGGCAGTTGGGTGAATATTAGTACCTTTC
CCTCAGNTNCATTAATTACCCCTGCCTACTCTGCACAAAAGGATNTAACAACAGTT
TCCTTTTTAATGGCCAGGTACAGCTGCTTATATGGANGGCATTTNTNAATGATAT
CCTTNATCACTGTCTTAATCATCACATNCTTAAAACAATCACTTTATTGTGTTAAG
GAAGATAAAAATGGCTGGGTTCAATTTCCGTTCTGGAAGAAATCGANTNAAAAGGT
AACCATTTAATAATGCANAGGGCANTTTCACTGCAGACCCTAATACTGGAAATTTT
TAAAAACAAATGAAAAACTTCTACTTTTTCTTCTAAGCTTACTTAACCACCCAAAT
TTTCCAGCCACATATCTTCCTAGTCTACAACTGCCTTTAACTTTAAGAGATGCTCA
AAAAAATGTAAATTCTCAAATACATTCTTATTACAATTACTGCTAACCT

Sequence ID 373

CCAGTGTGCTGGGATTACAGGCATGAGCCCTGCACCCAGCCTCTTAAACTGATCAT
ATGATATTGGTTCTCAACCAAGGGTGACTTTGCCCCCAGAGGATACTTGGCAATGT
CTGGAGATACTCAGTTGTCATGACTTGGACAGGTGCTACTGTCACCCAGTGGGTAG
AGGTCAGGGATGGTGCTAAACATAGGACAGCTGTCAAGAGAAAAGAATGTACCCAG
CCCCAAATGTCAGTAGGGCTGAGGTTGAGAAACCCAGCTGTAGCTGACGTGTGAAG
GACAGACTGGCCTGGAAGTGTGTTTTCTGCCCCTTTCCACCCCTGCATATTAGTTA
AGGCCAAAGGAAAAAAGGAATGCAGGAAATGCCCGTTAAAAATCTTCAAAACAATA
TAAAATGATCAATTCCACTAAAACCCTTTACACATTTAAGTATAAAGGTATTGGTA
GGAAAATTTGTTATTCACTGCTTTTCTCAGTGTCATGAAATAATTATTTCTGCTGT
CAGTTT

Sequence ID 374

AAAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAGACAT
TCTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAG
TGATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAA
ATGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTCTGAATAACAAA
AACAATCTTGGGGAAAAAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTCTAT
TTATAATTTACTACAAAGTTATAGTAATCAAAGTCGACGCGGCCGCGATTCCGGG

Sequence ID 378

CGACTGCGGCTCTTCCTCGGGCAGCGGAAGCGGCGCGGCGGTCGGAGAAGTGGCCT
AAAACTTCGGCGTTGGGTGAAAGAAAATGGCCCGAACCAAGCAGACTGCTCGTAAG
TCCACCGGTGGGAAAGCCCCCCGCAAACAGCTGGCCACGAAAGCCGCCAGGAAAAG
CGCTCCCTCTACCGGCGGGGTGAAGAAGCCTCATCGCTACAGGCCCGGGACCGTGG
CGCTTCGAGAGATTCGTCGTTATCAGAAGTCGACCGAGCTGCTCATCCGGAAGCTG
CCCTTCCAGAGGTTGGTGAGGGANATCGCCCAGG

Sequence ID 380

GCAATTTAATTTTTAATAACAAAGATACTGTATTTTAACATGGTGAAATATACTTG
GCTAAGTCCAGATTAAAAAAAAAAAGTATCTAGCCCAACAGTACAATTATACAGCT
TTGTACAGAACATTCCATAGATCAACAGAAAATACATTTGAGCGCAAAAATAAAAA
ATATTTAAGGAGAATCTCTAAGCAGCATTTTATTTCTGCAAAAGACATATCTTGTC
TGATTAAATATCTACAAGTGCTTTTCCTTTCAAAAATACATATATTCTTAATAGAC
TAAGTCATTAACAATGACCTGGTAATTCTTTCACTTCAATTTGAATGATTTATAAG
CTAAATCTTCAACCACAAAAAGGTTTTTATTTGTATTAAGATGTTACCACTTTTGA

CAAAAAGCTTAAAATATTTTATATTTCAAAGGAAAATTAGCAACATAACTTTACAA
TATATTCTATGATATTTTGATTGTGAGGGCTACTCTATTTAAAACTGATGATCTCT
GTTGTGTTGCTCAGATGCAGGAAAGCAGCAAAA

Sequence ID - 381 nt: 534

GACTTANATCTAAATGGACCACATTCTCTACTTAAAAAAATGCTATTAACCATGTG
ATCTTCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGAT
ATTCTTTGAATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTG
AGGACAGAGGTGCTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAG
GAGGTAAACCCCACCCTCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAAC
TCTTAAATGTGAGAAATGCTTGAAGATTCTAGTCATCTGAAGAAAGTCTCTTTATT
AAAGATTTTCATAAAAGAGACCAAAGCAGACAAACAGAAAAAGACATCTTGGGGAA
AAAAACAAGGATAATGGGAAGAGAAGGAAAGTTTTAAAAATTATCAATATCCTCAG
GGGGACAAAATATTATATCCTATAAAGACAGATTTTTATTTTTTAAAAAAATAGAA
AGCAAAACAAGCTCCTAAAAATAAAGTTTG

Sequence ID - 382 nt: 444

GTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGC
ATTTGTGCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACA
TGCCTTGGTTCAAGGGATGGAAAGTCACCCGTAAGGATGGCAATGCCAGTGGAACC
ACGCTGCTTGAGGCTCTGGACTGCATCCTACCACCAACTCGTCCAACTGACAAGCC
CTTGCGCCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTACTGTTCCTG
TTGGCCGAGTGGAGACTGGTGTTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCA
GTCAACGTTACAACGGAAGTAAAATCTGTCGAAATGCACCATGAAGCTTTGAGTGA
AGCTTTTCCTGGGGACAATGTGGGCTTCAATGTCAAGAATGTGTCTGTCAAG

Sequence ID - 383 nt: 566

CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATG
CTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGAT
ATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGC
ATTACATTTGGAAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA
CTGACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAG
CAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGACCAACTTGCGCAAGATGGG
AGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGCACACCCTGGGAGACA
GTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTGGGGTGACTTCC
CTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCTATAAGTT
GTACCAAAACATCCACTTAAGTTCTTTGATTTGTCCATTCCTTCAAATAAAGAAAT

TTGGTA

Sequence ID 384

TTTTGGGGTTTATATATAAGCCTGGTTCTTGCTGAAACTGCTTATGTTGATAACCA
GTTAGTGAGTTCCTCTCTATTGACTTGCTGGGAAGTTTATAGAGACATTTTTTATG
CATTCAGAGATTTCAGTACAAATCTTGAAAAAGGGACATTTAGGCCGGGCGCGGTG
GCTCACATCTGTAACCCTAGCACTCTGGGAGGCTGAGGTGGGTGGATCATGAAGTC
AAGAGATAGAGACCATCCTGGCAAAAATTAGCTGGGCGTGGTGGGGTGCGCCCGTA
GTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAGCCCGGGAGGCGGAG
GTTTCATTGAGCCGAGATAGTGCCACTGCACTCCAGCCTGGACAACAGAGCGAGAC
TGTGTCTT

Sequence ID 386

CTAAGGGTTTAAAGATGGAAAGAGGCATTGATGAACAGCTGGGGAAGGAGTAGTTT
GAGGTAGATGTGCAGATGGAATGAAGAGAAGGTCTCAAGAAGAGGGTGGAGCCAAA
GAGGGCTGCAGATTTAGAAGGCTAAAGTCTTTAGATGGCTTTGGATAGCCTGTTGT
ATCTTGGACCATGCAGGTTACAGTGGAGCATGGAGTGGGGACAGAAGTGGAGGAAG
GAACCAGGGAACATGGAGTGAGAAGCTAAAGGAAAGTGATGCAGTAGATACATGGC
TCTAAAGTACTCAGGACTTTCAGAGGCTTAAACATAGGGTGACCAACTATCCCACT
ATGCCTGATACTAAGGGCATTCCCTGGATGTGGACCTTTCATTCCCCAAATTAGGA
AAGTCTTGGGCATACCAAGACAAGTTGGCCACCCTACTCAAAAGTATGTAAGCTAA
CATATCTGTTCTCTAAGAGGTTAAAGCTGGATGGGGATACCAGATGTATGTACGTG
ATGCAGTTAAACAGCAATACAAGGGGGCAAGTCTACCTGATCGGCCAATTCAATGG
GA

Sequence ID 387

GAAGCCAAACCAAAGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGCA
GAGAAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCAA
CTGGAAGAAGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGATC
TGAGTGCCGACTACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTTA
ATGGTGTTGTCTTATTAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACTG
AGTAATCAGCTAGGCCCAGTCACTAGGTGAACAACTTACTGCTCCAATCAGCCTTA
GAGCAGGAATCAAACTCATGTCTCAGAAAAGTTATTAATTCAGCTTGTCTTGGGAC
TTCCTTCAGAGTCACTCTTGAATAGCTGAAATAGTAAATGTTAAATCTGTGGATGC
AAGTGTGTAAATTATTTTAGTCATCAGCTCTAATAAGATGGCCTTTGGGGAAATGA
GTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGGTCTACTATTTCTTCTGTAAT
ACTGATTTTTACCCCATCAGGGTCAGTCCCCAGAGGTTGTAAATGTGAAGCTTG-T

CTTTTTCTTTAATAA

Sequence ID 388
CTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGT
AGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTA
AAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACC
CTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAG
CCTGCGTCAGATTAAAACACTGAACTGACAATTAACAGCCCAATATCTACAATCAA
CCAACAAGTCATTATTACCCTCACTGTCAACCCAACACAGGCATGCTCATAAGGAA
AGGTTAAAAAAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAA
CATCACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTT
AACGGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAATTA
GGGACCTGTATGAATGGCTCCACGAGGGTTCAGCTGTCTCTTACTTTTAACCAGTG
AAATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCAAGACGAGAAGACCCTAT
GGAGCTTTAATTTATTAATGCAAACAGTCCTAACAAACCCCAGGTCCTAAACTCCA
AACCTGCATTAAA

Sequence ID 389
CGACCCGGAATTCGCGGCCGCGTCGACTGAGTTCTTGACAAGAGTGTTTTTCCCTT
CCCGTCACAGAGTGGGCCCAACGACCTACGGCACTTTGACCCCGAGTTTACCGAAG
AGCCTGTCCCCAACTCCATTGGCAAGTCCCCTGACAGCGTCCTCGTCACAGCCAGC
GTCAAGGAAGCTGCCGAGGCTTTCCTAGGCTTTTCCTATGCGCCTCCCACGGACTC
TTTCCTCTGAACCCTGTTAGGGCTTGGTTTAAAGGATTTTATGTGTGTTTCCGAA
TGTTTTAGTTAGCCTTTTGGTGGAGCCGCCAGCTGACAGGACATCTTACAAGAGAA
TTTGCACATCTCTGGAAGCTTAGCAATCTTATTGCACACTGTTCGCTGGAAGCTTT
TTGAAGAGCACATTCTCCTCAGTGAGCTCATGAGGTTTTCATTTTTATTCTTCCTT
CCAACGTGGTGCTATCTCTGAAACGAGCGTTAGAGTGCCGCCTTAGACGGAGGCAG
GAGTTTCGTTAGAAAGCGGACGCTGTTCT

Sequence ID - 390 nt: 523
GAATCCCTAGAAAAAGAGAATTCCCAACTTGATGAGGAAAACTTAGAACTGCGAAG
GAATGTAGAATCTTTGAAGTGTGCAAGCATGAAAATGGCTCAGCTACAGCTAGAAA
ACAAAGAACTGGAAAGTGAAAAAGAGCAACTTAAGAAGGGTTTGGAGCTCCTGAAA
GCATCTTTCAAGAAAACAGAACGCTTAGAAGTTAGCTACCAGGGTTTAGATATAGA
AAATCAAAGACTGCAAAAAACTTTAGAGAACAGCAATAAAAAAATCCAGCAATTAG
AGAGTGAACTACAAGACTTAGAGATGGAAAATCAAACATTGCAGAAAAACCTAGAA
GAACTAAAAATATCTAGCAAAAGACTAGAACAGCTGGAAAAAGAAAATAAATCATT

AGAGCAAGAGACTTCTCAACTGGAAAAGGATAAGAAACAATTGGAGAAGGAAAATA
AGAGACTCCGACANCAAGCAGAAATTAAAGATCCACATTTGAAGAAAATAATGTGA
AGATTGGAAATTTGGAAAA

Sequence ID - 391 nt: 566
CTTTGAAGAACTTTGCCAAATACTTTCTTACCAATCTCATGAGGAGAGGGAACATG
CTGAGAAACTGATGAAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTTCAGGAT
ATCAAGAAACCAGACTGTGATGACTGGGAGAGCGGGCTGAATGCAATGGAGTGTGC
ATTACATTTGGAAAAAAATGTGAATCAGTCACTACTGGAACTGCACAAACTGGCCA
CTGACAAAAATGACCCCCATTTGTGTGACTTCATTGAGACACATTACCTGAATGAG
CAGGTGAAAGCCATCAAAGAATTGGGTGACCACGTGACCAACTTGCGCAAGATGGG
AGCGCCCGAATCTGGCTTGGCGGAATATCTCTTTGACAAGCACACCCTGGGAGACA
GTGATAATGAAAGCTAAGCCTCGGGCTAATTTCCCCATAGCCGTGGGGTGACTTCC
CTGGTCACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCTATAAGTT
GTACCAAAACATCCACTTAAGTTCTTTGATTTGTCCATTCCTTCAAATAAAGAAAT
TTGGTA

Sequence ID 394
GACCCGGAATCGCGGCCGCGTCGACCATTTTAGCCAAGGTGCCTCTATAGGGGTCA
AGACATCATGTGCCCAGACCTAAGGTCAGGAATGTCATATTTTTCTGTTAAAATCA
TTTTATTTCTGTGTATCTTACCTTTAAATCATTGTGGTTTACTCTGAGATTCTGTA
GTCCTAATATTGTATCATTGTGCTGTCTGCAAAACAACTTGAATCTATTTTGTTTG
CATCTTTTGTTACATGTAACGCAGCTGTACTTTATGTTCTTTGCAACTGTTTCCAT
TATGAGAACGCTGTGCTATTTACAAGGTTACATTTTTCTTGGCCAGGCGAGGTGGT
CATGCCTGTGATCCCAGCACTTTGGGAGGCCAAGGTGGGCGGATCACTTGAGGTAA
AGAGTTGAGACCAGCCTGGCTAGCATGGCGAAGCCCAGTCTCTACTAAAAATACAA
AAATTGGCCGGGTGAAATTAGCCGGGCGTGGTGGTGTGTGCTTGTAATCCCAGCTA
CTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCCGGGAGGCAGAGGTTGCAGTGA
GCCAAGATCANGCCACTGCACTCCACCTCGGGGTCAAGAGCGAAACTCTGTCTCAA

Sequence ID 395
CCGTTTTAGTCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCTGCCTCGGCC
TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCGTAAATCAGGTTT
TTTAAATGTTTGCCAAACCTTATCACTGACTTTTATAACAAAATTATTTACTATAA
TCATTAGGGAATATTTAAGTTCTGCTAATACTTAAAATTGCAGAGTGCTAAAACCA
GCAGTGAGTTTAGAATCAAGCTAAGCTTTATTGTTGCTACTATTTGAGGCATATTA
GTTGACTGGTGTTCATATGCAAGGCAGTCTACTGGGTGCAACAAGGGTTAGAAGGA

TATTTTTAAAAAACTGACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTC
TGCTCTGTTGGTTAACTCCTCGTAAGGAGGTCAATTAAAATGCTGTAGTGTTGCAA
GGGAAGGAGAGGAAGAATCATATTCCTTCACTAGCAGGATCAAGAAAGCTTTTATA
GAAATATACAAAATCTTCACTTCTTGAAGGATTGGTAAAATTTAATAGCCAACATT
GGGCACTTATTCATTCTCTGAGTAAATATTTATTGCAT

Sequence ID 396
CTTAAATCTAAATGGACCACATTCTCTACTTAAAAAAATGCTATTAACCATGTGAT
CTTCTCAGTCATGAGGTAATCTGGTGACTACCCTTCCTCAAAGCCAGTTGGGATAT
TCTTTGAATAGAGTAAAACAGTGTTTCTAGGCTGGGAGACACCAGACATAGTTGAG
GACAGAGGTGCTAGAAAATAGGAAGTTTAAAAGCATGTGCGGTGATGCTCAGAGGA
GGTAAACCCCACCCTCATGCTCATAGCTTCCAATCATTTTCTCTAGTTCTTAACTC
TTAAATGTGAGAAATGCTTGAAGATTACTAGTCATCTGAAGAAAGTCTCTTTATTA
AAGATTTTCATAAAAGAGACCAAAGCAGACAAACAGAAAAAGACATCTTGGGGAAA
AAAACAAGGATAATGGGAAGAGAAGGAAAGTTTTAAAAATTATCAATATCCTCAGG
GGGACAAAATATTATATCCTATAAAGACAGATTTTTATTTTTTAAAAAAATAGAAA
GCAAAACAAGCTCCTAAAAA

Sequence ID - 397 nt: 534
GACCCGGAATCGCGGCCGCGTCGACGGAAGCTCCTGCCCCTCCTAAAGCTGAAGCC
AAAGCGAAGGCTTTAAAGGCCAAGAAGGCAGTGTTGAAAGGTGTCCACAGCCACAA
AAAGAAGGAGATCCGCACGTCACCCACCTTCCGGCGGCCGAAGACACTGCGACTCC
GGAGACAGCCCAAATATCCTCGGAAGAGCGCTCCCAGGAGAAACAAGCTTGACCAC
TATGCTATCATCAAGTTTCCGCTGACCACTGAGTCTGCCATGAAGAAGATAGAAGA
CAACAACACACTTGTGTTCATTGTGGATGTTAAAGCCAACAAGCACCAGATTAAAC
AGGCTGTGAAGAAGCTGTATGACATTGATGTGGCCAAGGTCAACACCCTGATTCGG
CCTGATGGAGAGAAGAAGGCATATGTTCGACTGGCTCCTGATTACGATGCTTTGGA
TGTTGCCAACAAAATTGGGATCATTTAAACTGAGTCCAGCTGCCTAATTCTGAATA
TATATATATATATATATCTTTTCACCATAA

Sequence ID - 398 nt: 512
GGGGAGCCCCCTCTTCCCTCAGTTGTTCCTACTCAGACTGTTGCACTCTAAACCTA
GGGAGGTTGAAGAATGAGACCCTTAGGTTTTAACACGAATCCTGACACCACCATCT
ATAGGGTCCCAACTTGGTTATTGTAGGCAACCTTCCCTCTCTCCTTGGTGAAGAAC
ATCCCAAGCCAGAAAGAAGTTAACTACAGTGTTTTCCTTTGCACCGATCCCCACCC
CAATTCAATCCCGGAAGGGACTTACTTAGGAAACCCTTCTTTACTAGATATCCTGG
CCCCCTGGGCTTGTGAACACCTCCTAGCCACATCACTACAGTACAGTGAGTGACCC

CAGCCTCCTGCCTACCCCAAGATGCCCCTCCCCACCCTGACCGTGCTAACTGTGTG
TACATATATATTCTACATATATGTATATTAAAACTGCACTGCCATGTCTGCCCTTT
TTTGTGGTGTCTAGCATTAACTTATTGTCTAGGCCAAAGCGGGGGTGGGAGGGGAA
TGCCACAG

Sequence ID 399

TTTTGGCATTACTTAATCCAATTATAAAAACTGAATTTTTAAAAAACAGCACTTGT
TTTTTCTTCCAAGATTAATTTGAATTTTTTTATGGACATTAGAAAACATTGCAGTT
TAGTCATAATCAAAAATAAATCTTGAGGCTGGTAGAGCAGCTTTGTTGCTGTTTAT
ATTTTTATTGCTTACTGGATTTCAGTGTTACCTAGTGCCATCAGTTTGGTATTTTG
CCACCTTGCACATTCAGTGATGTTTGATTTTTCTTTTTCCTTTTTTTCATATTACT
TTTAAATCCTGAATAGTTTGTGGCAGCTGGAGATCACCTAGTCCACCACTGTCCAA
CATGGCAATGGTAAGTAATATTGAGTAAAGAATAGAAAATTAGTAAAATGCATGGC
TTCAGAATTATAGCAATTTGCAAAATAGGTTAATGGATGAAAATTAGAATGACCAG
TTTAACTTTCCCCCCAGCAGATTCTTCTGTTAAACAATGCCCCTTCAAAATAAAGG
AAGAACAAGTGGGTGTTATACCTATGTTATTTGGCTATGTTAGCACAATATGATGG
ACTAATTTGAGAAAAAGCATTTACTTCCTTTACTATTACTTCTTTTCTTTATAGGG
CTAAGTCTGCCTTCTGGGTCTTTGAA

Sequence ID 400

GAAGAAGCGCGAAGAGCCGTTAGTCATGCCGGTGTGGTGGCGGCGGCGGAGACTGC
GGGCCCGTAGCTGGGCTCTGCGAGGTGCAAGAAAGCCTTTGAGGTGAAGGTGTATG
AAAGTCATCATAACAGATGTTTTCCAAAAACTTGTAGAAGGTTGTGAAAAAACTAC
TAGGATCACGCGGCATGTATTGAGCATATAGGTTGCTGTAGATGAATGTTCTTAGC
TGTCATGTTTAAAAATACTTCTGCTTCGTTACCTCAAGTGTGGCATGCAGCATTTT
GGAAGGAAAATTGAAGACGTGTTCAAGAAAACATGAACAGAAGCAAATGATGAAAA
TGAGCATTTTACTTGATGTTGATAACATCACAATAAATTATGGAGAAAAATACATA
TTTGGCTAACTTTTAATTGCTGAACAATAAAGTGTTTTCTTTTAAATCNAAAAA

Sequence ID 401

GAAGCCAAACCAAAGGGAGCTTCTACTTCATGATGCCATTTATGTAAAGTTCAGGC
AGAGAAAATCAGTGGTTTAAGAAGTTAGAATAATGATTATCTTTGGAGGGATTGCA
ACTGGAAGAAGTCATGATTGGGATTTCTGGGTCCTAATAGTGCTCTGTGTCTTGAT
CTGAGTGCCGACTACATGAGTGGTTAGGTTTGCAAAATTCATTGAGTTATGCACTT
AATGGTGTTGTCTTATTAGAGCTGATGGAGGAGAGAGGGCTTCAATTTGCACAACT
GAGTAATCAGCTAGGCCCAGTCACTAGGTGAACAACTTACTGCTACCAATCAGCCT
TAGAGCAGGAATCAAACTCATGTCTCAGAAAAGTTATTAATTCAGCTTGTCTTGGG

ACTTCCTTCAGAGTCACTCTTGAATAGCTGAAATAGTAAATGTTAAATCTGTGGAT
GCAAGTGTGTAAATTATTTAGTCATCAGCTCTAATAAGATGGCCTTTGGGGAAAT
GAGTATAAGGTCACGAAAATGAAATGGCAAGAAGGAGGTCTACTATTTCTTCTGTA
ATACTGATTTTTACCCCATCAGGGTCAGTCCCCAAAGGTTGTAAATGTGAAGCTTG
GTCTTTTTCTTTA

Sequence ID 402
GACCCTATTCTCAGGATGAAAATAATACACTAGTAATAGTCTGCTCTGTTGGTTAA
CTCCTCGTAAGGAGGTACAATTAAAATGCTGTAGTGTTGCAAGGGAAGGAGAGGAA
GAATCATATTCCTTCACTAGCAGGATCAAGAAAGCTTTTATAGAAATATACAAAAT
CTTCACTTCTTGAAGGATTGGTAAAATTTAATAGCCAACATTGGGCACTTATTCAT
TCTCTGAGTAAATATTTATTGCATGCTTATCTTGTATCAACATTGNGATGAAAGCN
CAAGAATGAAAGAGGAGGGAGAATGTTTANAGAATAAGGCTGAAACACAGATTTTG
TAGGGAGCGTAGGGGAGACTGANAAAACAG

Sequence ID 403
AAGACACCTGATAGATTGTCTTGTATTATTTTTCCTTTGCCTTCTTACAATCTCAG
TGATTAGAATTGGGCTGAAAACAATACATCAAATTCTCAGCAAAATCCTTATGGGT
TGCTGGATACCGAGGGTTTTTAAGATCTTTAGACTTCACTATATAGAACAAATGTT
GAATGGGAATTTTCTTTATTTCTATANCGTTTNG

Sequence ID 405
CCCGGAATCGCGGCCGCGTCGACGATGAGCATTTTTTCATGTGTCTTTTGGCTGCA
TAAATGTCTTCTTTTGAGAAGTGTCGGTTCATATCCTTTGCCCACTTTTTGATGGG
GTTGTTTTTTTCTTGTAAATTTGTTTGAGTTCATTGTAGATTCTGGATATTAGCCC
TTTGTCAGATGAGTAGGTTGCGAAAATTTTCTCCCATTTGTAGGTTGCCTGTTCA
CTCTGATGGTAGTTTCATTTGCTGTGCAGAAGCTCTTTAGTTTAATTAGATCCCAT
TTGTCAATTTTGGCTTTTGTTGCCATTGCTTTTGGTGTTTTAGACTTGAAGTCCTT
GCCCATGCCTATGTCCTGAATGGTAATGCCTAGGTTTTCTTCTAGGGTTTTGATGG
TTTTAGGTCTAACGTTTCAGTCTTTAATCCATCTTTTAAAAGTCTCTTCACAGTAC
ATGAGTAGTAGTGACACCAATAATGTCAGAGCAGGGAACTCCCAGGTTCTGCCCAT
CCACAAAAACAACAAATAAGCTGGCAAAAACTTTAAGAATCAACTTTTGCAGATCT
CTGAAATCTAGTCAAAACTTAAACAGAGGAAAGATTAATAAAGACNGGCTGCCTGA
GATAACACTAACACACAC

Sequence ID 406
CATCAAATAAATAAATAAATAAATTTTAAAAGTCACAGCATTGAATTTTTAAATGT

TTGGGATGATAAAGCACCTGCTTATCATGAAGCTANAGAAATTCAATGACACGTTT
GCCAGGGTCTTTGCTAGTGATGTTGGAACAAGTCTGTAATGCTGATGAAACATCAC
TGTTCGGGCATTATTGCCCCAGAAAGACACTGACTGCAGCTGATGAAACAGCCCTT
CCAAGAATTAAGGATGCCAAAGACCAAATAACTGTGCTGAGATATACTTACGCAGC
AGGCATGCATAAGTGTAAACTTGCTGTTATAAGCAAAAGCTTGCGTTCTCACTGTT
TTCAAGGAGTGAATTTCATACCAATCCATTATTATGCTAATAAAAAGGCATGGATC
ACCAGGGACATCTTTTCAGATTGGTTTCACAAACATTTTGTACCAGCAGCTTGTGC
TTACTGCAGGGAAGCTGACTGGATGATGACTGCAAGATTTTGTTATATCTTAACAA
CTGTTGTGCTCATCCTCCAGCTGAAATTCTCATCAAAAATAATGTTTATGGCTCAC
ACCTGTAATCTCAACACTTTGGGAGGATTGCCTGACCCAGGAGTTCAAGCCCACCC
TGGGCAACACAGCAAGACCCAACCTNTC

Sequence ID 407

TTTTAAAAATCATAAAACGTTTCTTACAAAAGAGCATTACATTNTGCACACTGCTC
TGAACAGATGCCAGGGACATGTGGACTATTGTTACTTTTCCTCCCTGTCCCACCCC
CCAAATGTTACAGTGACCACAAAGCAAGGTGTTCACAATAATTACATGGGGGGAAT
TTTTTAAACCACCAACAATAACGAAAAATAAAATCCACTCACTCTGCTGCTGTTTC
AAAATTTCAATGTTAGTTTTTGCACGCCCTTCCCCCCCCCAACCCTGTTTGTAAGG
AACTAAAACATTACATCTGGTGAACAGCAAAGATTTCACTACACCTCAAATGCAGA
ACACCTATGAAGCAGAGGAATGTTGGCTTTTTAAACAGAAGCAGATAAAAAAAAAA
GATGCAGGACTCCTTCAGTTCTTCACTAGTCTTAGAAAAACTTTCCAGAATACTGC
TTCACACTATAAAAAAGAAAAAATATCTTGCATTAGAATCCTTCAACATCTGCATA
CTGCTTCACACTGTTCGTTTCTAGGAGCACTTTGTCACAGGACACTTCTGCTTATA
TTTCTTTAATCAGAACTTAGTTGGATGGGCCGGGCATGGTGGCTCACGCCTGTAAT
CCCAGCACTTTGGGAGGCCGAGG-GGGTGGATCACC

Sequence ID 408

CCATCTCCAAATTTAGTATTCATTCTGTTTAGCATATTATCAGTTGCCATCTATTT
GTTTTAACTGATTACTTGAATCTGATTAAACATCACAGAAATGGGCTTTGATAAGA
ACAATATTGAATAAGAAATTTTAAATAACAAAACAGCTTATAGAAAAATTCAGCAT
AACTTTTCCATCACCTTCACCACCCTTGCCTTTTATTATCCTGTCCTGTATCACTG
CTTTCTGTTAGCAGTGTTGTGTGAGTTAGGATTTGGGCAGGAAAGCAAAAGCAACC
ACCCGTCATTTTCCCAGAATGAAGGGTTTGACGTAGGATGTAGACTTTGTATAGTA
GTTGGGAGAGCTGTGGGAGTGAAGGTCAGGGATGTCACCTACAGAAGTCAGGGAAT
CTGCCACCAGAGATCCTGCATCAGAAACAGCCAACAGCGTGCTTCTGAAGAACTAG
TGGGGAAGTGGCTATAATTCTTAGGAATCCCAGCAAGTCCGCACCACTGTCTCAGT
CTACAGCAGTGGAGAAAGGGGTTTCCAGGAGCTCTCTGGAAAGTTCCTGCCCACAC

TTTGCAACAATCTTCAGAGGATAATGGGCTTCTCTTCCAGCTTCCACACCCAACAA
GAGTGCCTTTCATCGGCCAACTCTAACCTGGAACCCTATGGCAGAGGGGATTTAGG
AGACAGTTTGTNATGTCTGTGGAATGCAAATGAANANGTANCAATGCTTANTTGAC
AGCGGNCATACACAAATNTNGAAA

Sequence ID 409
GATCCGTNGACT

Sequence ID 410
CTCTTCCCAGCCCCTGAGCCCAGCCCCTTCCCAAGTGGTGCCAGACAAAAAACTAC
ATGGCCCTTTCGTGTCTTGGGGGTGGAAAGGGAGGGATGAATTGGGGTGATAGAAC
CCTGGTGAATTCAGAGTAATCTTTCTTTAGAAAACTGGTGTTTTCTAAAGAAACAG
GATAGGAGTTTAGAGAAGGCACCAAAGCTTTCACTTTGGTTTGGCACCAGTTTCTA
ACCATCTGTTTTTTCTACCCTAGCTATCTTTTATTGGTAAAATATAAATGTATAAT
TATGTTTGTAGAGCTTTACCAAGGAGTTTCCCTCCTTTTTTGTTTGTTGATTAGCA
AATTTTTGATTCTCCATTTTCCAAAAGTAAGAGACTCCAGCATGGCCTTCTGTTTG
CCCCGCAGTAAAGTAACTTCCATATAAAATGGTATTTGAAAGTGAGAGTTCATGAC
AACAGACCGTTTTCCATTTCATCTGTATTTTATCTCCGTGACTCCACTTGTGGGTT
T

Sequence ID - 411 nt: 505
TGGAGCTGAAAAATTCCTATTACCTAGGGGCATCACAACGCATTGCATTTCGCCCG
TGTTTGGGATGATGCTGGTGTAAACCTACTATGCTGCCAGTCATGTAAAAGTATAG
CACACACAATTAGTAGGTAATGCTTGCAAATAATAATGAAAGACTCTGCTACTGGT
TTATGTATTTACTATGCTATACTTTTTGTCATTACTTTAGAGTGTACTCCTACTTT
TTTTTTTTTTTTTTTGAGATGGAGTTTCACTCTTGTCCTGTAGGCTGGAGCGAAN
TGGCGCGATCTCGGCTTACTGCAACCTCCACCTCCTGGGTTCAAGCGATTCTCCTG
CCTCANCTTCCCAGAGTAGCTGAGATTACAGGCATGCACCGCCACGCACGGGTAAT
TTTGTATTTTTGGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCACCAACT
CCTGACCTCAGGTGACCCGCCTCCTCACCTCCAGAGTGTTGGGATTACAGGNGTGA
G

Sequence ID 412
ATAAAAATTAGCTGGGGGTGATGGGCCCTGTACCCCAGCTACTCGGGAGGTGAGGT
AGGAGAATCACTTGAACCCGGGAGATGGAGGTTGCAGTGAGCCAAGATCGTGCCAC
TGCACTCCAGCCTGTGTGACAGAACAAGACTCTGTCTCAAAAAAAAATAATAATAA
TAATAATAATAAAAAGGAATAACATAGCTAGGAATAAATTTAATCAAAGAGGTGAA

AGACTTATACACTTAAAACTACAAAAAAAAAATCACTGAAGGAATTATAGACCCAA
ATAAAAATAAATAAAAAGACATTCTGTGTTTTAGGGAAAGAAGACTTAATATTGTT
AAGATGTCAATACTACCCAAAGTGATCTACAGATTCAACATAATCCCTATCAAAAT
TCCAACAGCCTACTTTGTAGAAATGGAAAAGCCAATTTTCAAATTCAGATGGAATT
GCGAGGGGTTCTGAATAACAAAACACAATCTTGGGGAAAAAAAACAAAAAACAAAG
TCAAAGAACTCACACTTCTCTATTTATAATTTACTACAAAGTTATAGNATCAAAGT
CGACGCGCCGCGATCCGGGC

Sequence ID 413
CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACA
CGAAAATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAA
AGTAAAATCAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTA
ACAAAAAGAAAGAAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATG
TACCTTATTCCCACACACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATAT
TACTTTGTTTAAAATAAGATGCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAA
TTTAAAAACTCCTCTTCACGATTGATAGCAAAATCAGAAACGTTAGGGCACCAGTG
AGTTGAAAAAAACTGGTCTTAAGTTGGAAAAACTATTATTAATAATATTATCCTATC
CATCCATATCTATTGAAATTGTCAGGTCCATAATTTCATTTTAATTAATTATAGGA
AAGAAGAAAAGATAATACCCATTTGTTCTAT

Sequence ID 414
CTCAGACTCTTTCTGCCCTAATGGCCATTACTATCCAGTCTGTATTGCTACAAGGG
ACCCACTGGTACCCCTTTTAGATTCTATCAAAAGGAACAGGGTTTTCCTAGAGGCA
GGCAGCCTGGTGGTATGGCACAGCAGAAGCTTACTGCTAATGAAATGGGAACCTCC
CCCTCCCTTGTGGTTTCAGCACAGAACCTGAATGCCAGGAAAAATTCCTGGGCCAA
GAAGCTAAAGCTAAAGAAACCTTCCTTTTTTCAACGTTTTTTTTCTTTCAAACTG
TAGGGTCACTTTTGATTGAGGCAAAGGGGTCCTACTGTAAGTGGAAAAGACTCACT
CCCCTAACATAAGTTTTCACTGTGGTGGGATGGTGCCGCCCGATATGCTTGATATG
CTTTTCCTTCCACATGTTAAGCTAGGAAACCTAACAGGATGTCAGCAGGGCAGTTA
ACTCTGGACTCANAGCCCTCAAGGGCATGTGGCANAACCTCATGGCATNCAAGACC
A

Sequence ID - 415 nt: 596
GTATAATTGATTCTTTTGAACCTAAAGTATAAGACTTCACGATTAGAAAAAAATTA
TCCAAAGACTAATGTAATTAAGTGAGGAAAAGGTGCTGGAGGAACTGGATAACCAC
ATGGAAATGTATGAACCATGACCTCTATGTCACATACTATATATAAAACTTAATTT
GAGGTGTATCACAGAGCTAACTGTGGGGGCTAAAACGTTGAAGCCTTTGGATGGCC

GCACAAGAGATGTCTGCATTCATAACCTTGGGGAGGGTATGAACATTTCTTGGTAA
CATGCAAAAAGCACTAACTGTAAAAGAGAACAGTTGGTCAGTTGAATTTCATGAAA
CATTGTAAACTTCTGCTAAACAACTGACACCATTAAGAATGTGGAAAAAGGCTGGG
CACAGTGGCTCATGCCTATAATCCCAGCATTTTGGGAGGCCGGGGCGGGAGAATCA
CTTGAGGCCAGGAGTTTGAAACCAGCCTGGGCAACATGGCAAGACCCCGACTCTAC
AAAAATATTTTTAAAAATTAGTTGGGTGTGGTGATGCACTCCTGTAGTCCTAGCTG
CCAGGANGCTAAGGNGGAAGGATCACTTAACCCTGG

Sequence ID 416
CTGGTGGCGGCGGTCGTGCGGACGCAAACATGCAGATCTTTGTGAAGACCCTCACT
GGCAAAACCATCACCCTTGAGGTCGAGCCCAGTGACACCATTGAGAATGTCAAAGC
CAAAATTCAAGACAAGGAGGGTATCCCACCTGACCAGCAGCGTCTGATATTTGCCG
GCAAACAGCTGGAGGATGGCCGCACTCTCTCAGACTACAACATCCAGAAAGAGTCC
ACCCTGCACCTGGTGTTGCGCCTGCGAGGTGGCATTATTGAGCCTTCTCTCCGCCA
GCTTGCCCAGAAATACAACTGCGACAAGATGATCTGCCGCAAGTGCTATGCTCGCC
TTCACCCTCGTGCTGTCAACTGCCGCAAGAAGAAGTGTGGTCACACCAACAACCTG
CGTCCCAAGAAGAAGGTCAAATAAGGTTGTTCTTTCCTTGAAGGGCAGCCTCCTGC
CCAGGCCCCGTGGCCCTGGAGCCTCAATAAAGTGTCCCTTTCATTGACTGGAGCAG

Sequence ID 417
GCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCCGCAGATAAGTTT
TTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGG
TTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATT
TTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGG
TTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTAT
TTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGG
GCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAA
AGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGA
AGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTAAAGC
CTAGTTAACGCATTTACTAAACGCAGACCAAAATGGAAAGATTAATTGGGAGTGGT
AGGA

Sequence ID 418
CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTAT
GTAATGCAAAATTTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTT
GAATGATGAGCCTTCGTGCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATG
TATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTA

CACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTATAAAAAA

Sequence ID 419

CCCGGAATCGCGGCCGCGTCGACGGGAGGTGATAGCATTGCTTTCGTGTAAATTAT
GTAATGCAAAATTTTTTTAATCTTCGCCTTAATACTTTTTTATTTTGTTTTATTTT
GAATGATGAGCCTTCGTGCCCCCCCTTCCCCCTTTTTTGTCCCCCAACTTGAGATG
TATGAAGGCTTTTGGTCTCCCTGGGAGTGGGTGGAGGCAGCCAGGGCTTACCTGTA
CACTGACTTGAGACCAGTTGAATAAAAGTGCACACCTTATAAAA

Sequence ID 420

CTTCATTTGAAATGGTTGAATCTGCTGTGTAATAAAGTGGTTCAACCATGATTAGG
AACTGAAATTTAGTAGAAGAGGGAAAAGGAGTTAATGTAACAAATTATTTTAGCTA
CAAACCCCGGTAATAGAGCACTTGGGGGATGGGATGGGGTGGGTTGGTGAGACAAT
CAGAATGGTAAATTGATTAAATGCTCCTAACCCTGTAATTTTGTGCATAGAGCACC
CTATGCTGTGGAAATAACTGTTCTTAGATTTCATTGTAACTGGACTGTTCAGGTTG
CCCAGAGGGAAAGAACATTCCTAATTCTAATAAAATAAACTTTTATTTTGTTTA

Sequence ID 421

TGTCATTGAATCTGCTTGTTACTTAAATGCTAAACTCAATTCTGTAATTCAATAGG
TGCACCTCTCTGAGAAACATAAGAGACAATGAGGAAAAGGATTCAGCATTCCGTGG
AATTTGTACCATGATCAGTGTGAATCCCAGTGGCGTAATCCAAGTAAGATGTTCAC
AAAGATTTGTTTTTAATGTCTAATTAATAAAATTTTAAAGGAAGAAACATTCTAAT
ACTTTAATTATAAAAAGTTAACTATTTTCAAAGGTATCAAAATACAGTTAAACCTT
TAAAATGTATATTTCTTAATATCTTGAAATTGTAATGCCTTTTTTTTTTCCTAAAT
TTTTTTTGTCATGAAATGAGATAGTAACAGCAGATTGGGACAACAAGGTTATATTC
TTGTCTTGAATCAGGCCATGGCTTCTTTCATCCAAATTTCAGACCTCATTTATTTA
CTTTGTCCCTGCCTCCCATCCCTGGATATCAGTTTGTGGATATCTACAGTTAATAG
AGTGACCAAATAGTAGGAATACTGTCTCTCTATTCTGAATAAAATCTTTGAATCAG
ATTTAGAAATAATGAATAAAATACAAATCAGCCATTGAAATTGCTCTAATTTTGAG
AGCTTATGATTTATTCATCTTTGGTTTCCAAGTTCAAGTTATATGTAGACATTTTA
ATT

Sequence ID 422

GCTTCCTAGGTGAGGTCACGAGGAAACCTGCTGGCCAAGTGACCTGGCAGGGTGTG
GCCAGTGTGGCCAGGGCCGCCGAGCCTGCTTTCCTTCCCTGCAGCAGGAACCCTTC
TGGGGCTGTGATCCTGCGATGGTGCCTGGGTGGGAGTGGGGGTGGGGGGCGGGATG
GTCTCCCTACCTGCCAGCTTCTTGGTTTGAGGTGAGGACAGCCCCGGAAGCTCANA

CTTGGCTCCTGTCCATGTACTTGGGGCCATGAGCTCTGCAGGGACCTTGGAAAGAN
AGAGACGGGTGGTGTANGGCANGGGAAGGCATTGTCTTCAAACAGGAAAAAGCTGA
NAATGGAAACAGGCGAAACTTACCAAGTGTAACATCACCTGGAACTGAAGGAGGGT
GGGAAGGTTTTAATTATTTTAAAAATAGAGATGGGGTCTCACTATGTTGCCCAGGC
TGGTCTCAAACTACTGGGCTCAAGTGAACCTCCTTCT

Sequence ID - 423 nt: 387
TGTTTCTCNAGGGCGAGAGGCTGTCTTANAGCACCATTCTCTGGCCCTNGTCCCAT
GAGAAGGAACCGCACTCAGGAGCCACACTCTCCCACTNCCCTTGCCCANAAGACTC
ACAGAGGGCACGGAGCTGGCTGTGGTGAGAGGAGGTCCANCAAATTCCTGTCTGCA
NAAGGGTTCTGAACACCACCGCCTGGCAGCGTGCTGGAGGAGGGATTCCTCTTTTC
CTCACAGCAATTCTGACCAGAAACCTGTCAAATCAGGAATGGCTAAAATAAGACCA
GGGTATGAATGACCATCAGCCACAGTAAAACCAAGGCACAGCTCTCCTGAGCCCAC
CCAAGCTGCTGTGGCCCAGACTGGTGACATCACCTCAGGGCAAAAAAAAAA

Sequence ID - 424 nt: 420
CGCAGAATGGCTCCCGCAAAGAAGGGTGGCGAGAAGAAAAAGGGCCGTTCTGCCAT
CAACGAAGTGGTAACCCGAGAATACACCATCAACATTCACAAGCGCATCCATGGAG
TGGGCTTCAAGAAGCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATG
AAGGAGATGGGAACTCCAGATGTGCGCATTGACACCAGGCTCAACAAAGCTGTCTG
GGCCAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCAGAAAAC
GTAATGAGGATGAAGATTCACCAAATAAGCTATATACTTTGGTTACCTATGTACCT
GTTACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGAGAACTAATCGCTGAT
CGTCAGATCAAATAAAGTTATAAAATTG

Sequence ID 425
GGAAACTGATGCCAGTCAGAAACTCAGATCAAATGAAGGGGTGAAGAGAACCAGAA
TTGATCTCTCTGTAGGAGAATATAAATGACTTTTTTAAAGTACATATTTTCTGTGA
AAGACAGTTTTTTGTTTAATGCAAAAATGTTAACAATGTTTATATCATGTAGAAGT
AAAAGATCGTGAAACAGCACAGAGAACAGTAGTAAGACAGATTGAATTGCACTGTT
GTAAGATGATGAACTTACAATATTAAGTGAAGGTAGACTGTGATAGATTAAGGATA
TATATTGTAATCCCTAGAGCAATTGTCAAAGTGGTACAGGTAAAAAGCCAATAGAG
GTGATAAAATGGAATACTAAAAAATATCAGATGAATAATAAAGAAGACAGGAAATG
AGGAACAGTGGAACAGAATGAATAAAAAACAAGACCATTAACTTAATCATTAATAA
TTACTTTAAATGGGTTAAACATTATGGTTATAAGGCAGAGATTTTCAGACTAGATA
AAAGAGCAAGCTCCACTATATACTGTCTACAAGAGATATACTTTAAAGTGTATATT
ATATTTAAATATAAAGATTTGGAATAAATAAACCTAAGAATAAGCTTACTAGGGAA

GTGAAAGATCTGTACAACAAGAATTACAAAACACTGCTGAACGAAATCATAGGTGA
CCA

Sequence ID 426
GTCCCGGAATCGCGGCCGCGTCGACGTTTCCTCAAAATTTATCTTCCTGTTAATGT
CAGGCATGTATCTCCTTAGCTTGCCACAAATAACTATATATACCACAGACCTTCCT
TTGTAGGGCTAACAGTGTTGCATTGTAAGTGGAGGCCTCATAGATACCTGGCCTTT
TCCTACCTTATTCCAAAGATGGTTGCATCTTATAAATAATGTCATTCTTCAGCAAA
TGGTATGGAAATGAGATTGTAATGTCATTATTTCCTCTTTAAATAATCAGGACAAC
TCATGATACAAAGAGCTCTTCTCTATAAAAGGTGGGACTTTTTTTTTTAGTAATAG
CAAAAATAAAATTGTACCTCCTTAATCTTCTACAGAAAGATGGATTTCATTTTCAA
CATTAAGAGGTAGTTTTAAGAAGCAGTAGAAGTCAGCCTGGGCAGCATGGTGAAAC
CCCGTCTCTACAAAAAAGTTAGCTGGGCTTAGTAGTTGCAATCCCAGCTACTCTGG
AGGCTGAGGTTGGAGATCATCTGANCCTGGGGAGGTCNAGGCTGCAATGATACANT
GAGCCCTGATTGTGCCACTCCACCTGGTTGCAGA

Sequence ID 427
TTCCAATCTTCGTGTTCACTTTAAGAACACTCGTGAAACTGCTCAGGCCATCAAGG
GTATGCATATACGAAAAGCCACGAAGTATCTGAAAGATGTCACTTTACAGAAACAG
TGTGTACCATTCCGACGTTACAATGGTGGAGTTGGCAGGTGTGCGCAGGCCAAGCA
ATGGGGCTGGACACAAGGTCGGTGGCCCAAAAAGAGTGCTGAATTTTTGCTGCACA
TGCTTAAAAACGCAGAGAGTAATGCTGAACTTAAGGGTTTAGATGTAGATTCTCTG
GTCATTGAGCATATCCAAGTGAACAAAGCACCTAAGATGCGCCGCCGGACCTACAG
AGCTCATGGTCGGATTAACCCATACATGAGCTCTCCCTGCCACATTGAGATGATCC
TTACGGAAAAGGAACAGATTGTTCCTAAACCAGAAGAGGAGGTTGCCCAGAAGAAA
AAGATATCCCAGAAGAAACTGAAGAAACAAAAACTTATGGCACGGGAGTAAATTCA
GCATTAAAATAAATGTAATTAAAAGG

Sequence ID 428
TGCAGGATCCGTCGACTCTAGATAACATGGCTAGAAAAGAGAATGAAAAAGTTGGA
ATTTTTAATTGCCATGGTATGGGGGGTAATCAGGTTTTCTCTTATACTGCCAACAA
AGAAATTAGAACAGATGACCTTTGCTTGGATGTTTCCAAACTTAATGGCCCAGTTA
CAATGCTCAAATGCCACCACCTAAAAGGCAACCAACTCTGGGAGTATGACCCAGTG
AAATTAACCCTGCAGCATGTGAACAGTAATCAGTGCCTGGATAAAGCCACAGAAGA
GGATAGCCAGGTGCCCAGCATTAGAGACTGCAATGGAAGTCGGTCCCAGCAGTGGC
TTCTTCGAAACGTCACCCTGCCAGAAATATTCTGAGACCAAATTT

Sequence ID - 429 nt: 535

CACAGTACTCCATTTTGGGGTCCAAACTGTAATGCTCAAAATAATAAATGCTTACA
CGAAAATTATTTATTGAGAATATTCATATAAAAATTACCTAAAGCAAAGTAAAAAA
AGTAAAATCAAGGTGGTATATTTGAAGTGAATGGTGATTGGAAATTTTTAGCTGTA
ACAAAAAGAAAGAAAACAACTTTTTTTAAAGCCTCATTCTCTTTTCTTTCAAAATG
TACCTTATTCCCACACACTCTTGGGCTGACCTTTATTTTATCAATAAGCTCAATAT
TACTTTGTTTAAAATAAGATGCTTCAGCAAAAGTCATTCTCTCTTTAACCATATAA
TTTAAAAACTCCTCTTCACGATTGATAGCAAAATCAGAAACGTTAGGGCACCAGTG
AGTTGAAAAAACTGGTCTTAAGTTGGAAAAACTATTATTAATAATATTATCCTATC
CATCCATATCTATTGAAATTGTCAGGTCCATAATTTCATTTTAATTAATTATAGGA
AAGAAGAAAAGATAATACCCATTTGTTCTAT

Sequence ID 430

CAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTT
TTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGGTT
ACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTT
AAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTT
TCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTT
AAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGC
AATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAAAG
TTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGAAG
GTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTAAAGCCT
AGTTAACGCATTTACTAAACGCAGACGAAAATGGAAAGATTAATTGGGAGTGGTAG
GATGAAACAATTTGGAGAAGATAGAAGTTTGAAGTGGAAAACTGGAAGACAGAAGT
ACC

Sequence ID 431

CGCTGGGTGCCTGCAGCGCCTCCCTTGTCTCATATGGTGTGTCCAGCACTCTATTG
TTGTAAACTGTTGNTTTGNCTGACCTAAATTNTCTTTACTAAACANATTTAATAGT
TNAAAAAAAAAAAAANANCA

Sequence ID 432

TTTTAAAGTCATCTCTATAGGAAGGTGCTGGGCAGGGATCCCAGAGAAAGAAAGGG
TCCAAGACTCCATTAACTGCCCTGGATGAAGGGCACTGCTACAGCAGCTAGTACCA
GAGACTCTCCTATCTCACGGTTGAGGCAGACCCAGGATAGAATAGAGAATAAAAGG
AATGCTTATAGGAAACAATTTTGTATGGAATGCTAGATGGCCAAGCCTCAGCCTTT
GGTCCAGTGCAACCCTTGCCTCGCTTGTCAACAGTGAAAAATTAGTTTGGTTAGAA

GAACCATCTGGAAACACACCAGCTTCTGCTACCTTCATGCTCATTGTTAAAAAAG
ATTAACCAGTGTGAACATTCTGATCTGTTAATTCCAGGGACTGTTTTCTTTCCAAT
GGACTGTTTGTTGGTAGAATAACCCCCAAAAGCTCAAAGCTAAAATGCATCATCAG
TCCTAGTCGGCAGTTCCTTAAGAATGGACTGGCGGCGTGGTTGAGCTGATATGGAA
AAGCTGCACCTTCCTGCAGAAGATCAACTGACCTGCTATCCCACCCCAAATTTCAA
CCTGAGGTATATTTCAATGAAGGCAGGTAGCTGTGCTTCTCAGAGCA

Sequence ID 433
TCCCGGAATCGCGGCCGCGTCGACCCGCCGCCGAGGATTCAGCAGCCTCCCCCTTG
AGCCCCCTCGCTTCCCGACGTTCCGTTCCCCCCTGCCCGCCTTCTCCCGCCACCGC
CGCCGCCGCCTTCCGCAGGCCGTTTCCACCGAGGAAAAGGAATCGTATCGTATGTC
CGCTATCCAGAACCTCCACTCTTTCGACCCCTTTGCTGATGCAAGTAAGGGTGATG
ACCTGCTTCCTGCTGGCACTGAGGATTATATCCATATAAGAATTCAACAGAGAAAC
GGCAGGAAGACCCTTACTACTGTCCAAGGGATCGCTGATGATTACGATAAAAAGAA
ACTAGTGAAGGCGTTTAAGAAAAAGTTTGCCTGCAATGGTACTGTAATTGAGCATC
CGGAATATGGAGAAGTAATTCAGCTACAGGGTGACCAACGCAAGAACATATGCCAG
TTCCTCGTAGAGATTGGACTGGCTAAGGACGATCAGCTGAAGGTTCATGGGTTTTA
AGTGCTTGTGGCTCACTGAAGCTTAAGTGAGGATTTCCTTGCAATGAGTAGAATTT
CCCTTCCTCCCTTGTCACAGGTTTAAAAACCTCACAGCTTGTATAATGTAACCATT
TGGGGTCCGCTTTTAACTTGGACTAGTGTAACTNCTTCATGCAATAAACTGAAAAG
ACCATGCTGCTANTC

Sequence ID 434
TTCGGACGCAAGAAGACAGCGACAGCTGTGGCGCACTGCAAACGCGGCAATGGTCT
CATCAAGGTGAACGGGCGGCCCCTGGAGATGATTGAGCCGCGCACGCTACAGTACA
AGCTGCTGGAGCCAGTTCTGCTTCTCGGCAAGGAGCGATTTGCTGGTGTAGACATC
CGTGTCCGTGTAAAGGGTGGTGGTCACGTGGCCCANATTTATGCTATCCGTCAGTC
CATCTCCAAAGCCCTGGTGGCCTATTACCANAAATATGTGGATGAGGCTTCCAAGA
AGGAGATCAAAGACATCCTCATCCAGTATGACCGGACCCTGCTGGTAGCTGACCCT
CGTCGCTGCGAGTCCAAAAAGTTTGGAGGCCCTGGTGCCCGCGCTCGCTACCAGAA
ATCCTACCGATAAGCCCATCGTGACTCAAAACTCACTTGTATAATAAACAGTTTTT
GAGGGATTTTAAAA

Sequence ID 435
CTGCAATGTGCAATAGTTGCACCACTGCACTCCAGCCTGGGTGACAGAGTGAGAAC
CTATCTCTTAAAAAAAAAAAAAAAAAAAGGAAGAAGAGACATGAGAGGGCCCAAGT
CACTTGCTCACTCACTTTCCGTGTACATGTACCAAGAAAAGGCCATGTGGGAAAGA

GCAAGAAGGCAGCCGCCTTCAAGACAGGAAGAGAGCCCTCACCAGAAACTGAGCCA
GAACCTTGGAATTCCAGCCTCCANAACTGTGAGAAAAGAATTTTCTGTTGTTTCAG
TCCCCCACACTATGGCATTTTGTTACGGCAGCCTGAGCTAATACTCCTACTTTGTC
CTGCATTTACTTGGTCTTCCAGTTAGTTTTTAGACTTTGGGAATCAGAGCAGTCA
GTTGTCAGATTTTAGCTTACAGTTGTCCTACCTGTGCAACTGAAATTTCTTCCATT
TTAAACCAGAGCAGAGTTTTAGAGTCAAAAGAAACCAGATCTTTTAGTGCAGAAGC
TTTCCACTGTATTANAAGTGAGGAAGTTGGT

Sequence ID 436
AAAAAAACTCCAGAGAAGTTTATAGAAAGAGATGACATGTAAACCCTGCTGAAAAA
TAGTTTCATTTGTTAGAATATAATTGTCTTCCACTAAAAAAAGAAAAAAAAAAGCA
TTTAAGGCTCTAAGATCTCTTGAAGTACCACTTTTCCTGAATCCCAGAGTTTTTAT
GTGCATTATTTTTATGCGTTTGTAGTTTGATATGTTGTATTTATAAGTAGTTTTAG
CTTTCCATTATGAATTCTTCTTTGACCCATGAGTTATTTAGGTAAGTGTTTAAAAA
TTTACAATAGTTTATATATGCAAATATTATGTTGTTAGAGTTGGTTTTCATGTCAT
TTTTACATATACAGGGGCAGTTTCCCCAACTAAATTGTATATTCCTTAAAGCAGCA
CTCTTAAATTTTATTTCTGTGTCAATTTCTTGNCTGTGTTTCCTGGCATGGAATAC
ATGGCATAAAATTTGTTATGTAATTAAATGAAATATTATTATACTTTCTATTTTTT
AGAAAAAA

Sequence ID - 438 nt: 577
GTCGACAGGGATGACATAACTATTAGTGGCAGGTTAGTTGTTGGTCACTTTCAACT
CTGGGTTCAAGCGATTCTCCTACCTCAGCCTCCCGAGTAGCTGGGATTACAGGCAT
GCACCGCCACACCTAATTTTCTATTCTTAGTAGAGACGGGGTTTCTCCCTGTTGGT
CAGGCTGGTCTCGAACTCCCGACCTCAGGTGATCTGCCTGCCTCAGTCTCCCAAAG
TCCTGGAACCACAGACATGAGCCACCACGCCTGGCCCCTTTTAAAATATTTCTGCT
CATTGATGATGCACCCAGTCACCCAAGTGCTCTGATGGAGATGTATAAGGAGATGA
ATGCTGTTTTCATGGCTGCTAATACAACATTCATTCTGCAACCCCCAAATCAAGAA
GTAATTTTGACTTTCAAGTCTTATTATTTAAGAAATATATTTTGCAAGACTATAGC
TGCCATAGACCGTGATTCCTCTGATGGATCAGACAAACTAAAATGAAAACCTCCTG
CAACGTATTCATCATTCTAGATCCCTGAGGAATCGCCACACTGACTTNCACAATGG
GTGAACTGGGTTACAGT

Sequence ID - 441 nt: 552
AAACAAAATTATTCTCTGAGAGGGAAAGGACATTTGAGGGAAACATCAAATTTCCC
CATAAATAAATGAATGGAGTTTGCAGGAAGGTGAGGGTGAGCAGAGATGTGTGTGG

ACATCTCTGACCATCCATCGCTGTATTCAAATGGATTGTTTATTCCATTCTGGTC
TCAGGCATGACCACGTCCAGTGAAGACATTTGAGGCAGCACATCTCAGGACCCAGG
CAATAGACTGGCCCCAACTCAGGCTGGACTAAGGTGTGATTAATTCTTTGTTTTTT
GTGTGGAACAGCTCACCTTGTCAGACAGCCTCAGGGCATCTCTGAGACACAGGGGC
AGAAAATGACATTCATCTTTTGAGTCCTCATCCATGGAGTGCTGTGTTTGGGGGGC
TGCATCTGCTGAAGCGAGAACCCCATTCTGCCACCCCACCAGGATGCCCATTCTCC
AGGACTTCTCCAACTTACTATTAGACTAAACCAGAACAAGCAACAAACTGTATTTA
TGCAAGCAAAATTGATGAGAAAATTATATTCAAATAAAGCAAAAATTA

Sequence ID - 442 nt: 606
TCGTGCCACTGCACTCCAGCCTGGACGACAGAGTGAGACTCCATCTCAAAATAAAT
AAATAAATAAATAAATAAATAAATAAAAAAATAAAAAATACTTCTGCTATGA
AAAACCTAGTTGGTATTTTTGCTTATTTAATACTATAGAAATATGGTGATCTCATC
TTTAATAGAGTGCTTTTAAGGTCCCCAGTGATAATCTCCTAAAATCATGAACTTTA
AGAATTTATAATGTTAATATGAGGAAATGAAATCTGGATTATCTCACCACATATTA
TATAATTCATTAGTGACAGAGCAAGAACTCCAGGTCACCTGTCTATTCCATGTTTT
TCCTATCTGCCTTTAAATGTTGAGATACTACCCTTATCTCATGTGAATGGAGAAAC
TGCCTAAAATGCTAAAACTGACTCAGAGGCACCCAGACATAAGTGAAGTGTGATTA
GAAAATCCTGGTCAGTTGAGTCTTAGCCAAATGTGTACCTACTGTGTCTGCCTCTA
TCAAGTCAATGAAAACATGATCTGAGAACTGTAAGTCCATTTATGGAAAGGGTTGA
TTTANAGATATTTTGAACTTNCAGTGATGAGCCCCTTCTCAAATAG

Sequence ID 446
CGGACTCCTGTGCTAATTGTCAGCTTACATATCATTGTATAGAGACTGTTTATTCT
GTACCAAACTGATTTCAAAAGTACTACATNGAAAATAAACCGGTGACTGTTTTTCT
TCATAAAGTTCTGCGTTTGGCATCTTCACTCTTTCCAAAATGTATCTGTACATCAN
AAATGTCACTATTCCAAGTGTCTTTTTAGTGTGGCTTTAGTATGGCTTCCTTTTAA
TATTGNACATACATTGNATCTTTGTTTTATGGNAATAAGTAATAAAAATGTAGACT
TCATATTTTGTACAAAATGTCCTATGTACAGAATAAAAAAGTTCATAGAAACAGCC
NANAA

Sequence ID 447
AGGCCGAGGCAGGCAGATCNCNTGAGGTCAAGAGTTTGAGACCAGCNTAGCTAACA
TGGTGAAACCCCATCTCTACAAAAATATA-AAAATTAGCCTGG-GTGGTGATGGGC
ACCTGTAACCCCAGCTACTCGGGAGGCTGAGGTAGGAGAATCACTTGAACCCGGGA
GATGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGTGTGACAGA
ACAAGACTCTGTCTCAAAAAAAAATAATAATAATAATAATAATAAAAGGAATAAC

ATAGCTAGGAATAAATTTAATCAAAGAGGTGAAAGACTTATACACTTAAAACTACA
AAAAAAAAATCACTGAAGGAATTATAGACCCAAATAAAAATAAATAAAAAGACATT
CTGTGTTTTAGGGAAAGAAGACTTAATATTGTTAAGATGTCAATACTACCCAAAGT
GATCTACAGATTCAACATAATCCCTATCAAAATTCCAACAGCCTACTTTGTAGAAA
TGGAAAAGCCAATTTTCAAATTCAGATGGAATTGCGAGGGGTTNTGAATAACAAAA
CACNATCTTGGGGAAAAAAAACAAAAAACAAAGTCAAAGAACTCACACTTCTNTAT
TTATAAATTTACTACAAAGTTATAGTAATCNAA

Sequence ID - 448 nt: 329

TACGCACACGAGAACATGCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGA
GGAGAAGAGGAAACACAAGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCA
TGGATGTGAAATGCCCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAA
ACGGTAGTTTTGTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAA
AGCAAGGCTTACAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTG
AGTCAAGATGAGTGGGAAACCATCTCAATAAACACATTTTGGGTTAAAA

Sequence ID 450

GAGCAGTGGCATGATCACACCTTACTGCGGCCTCCAACCCCTGAGCTTAAGTGATT
CTCCCGCATTATCCTCCTGAGTAGCTGAGACTACAGGTGCATGCCACCATACACTA
CTAAATTTGGGTCGGGTGGTGGTGGTGATTTTTTAATATTTTTGTAGAGACAGGGT
CTCACTGTGATGCCCAGGCTGGTCTTGAACTCCTGGGCTCAAGCAGTCACCCACCT
CAGCCTCCCAAAGCACTGGGATTACAGGTGTGAGCCACCACACTGGCCAGCTTTGT
TTTGTTTTGATGACTAAGCTGCTCTTGCTAAAAGGGCTTCTCTCTGAACTTCCCTA
CCTTTCTTCTGTTTCCCTGGGCTAGGGCTCCATGTTGGCAGTCCTACTCCCAATTA
ACCTGGGGCTGTCTGGTTAACCTTTATAAGATCTGCAGTCATTGGGAGACCCGGGG
ACCAGGAATATTGTTGTTGAGGGAGCTACCCTGGAAAGTGGATGGGTGGCCAAAGG

Sequence ID 452

TTTGGCTTTGCCTCTAGGCATTAGATGTTATCTTTGGAGGCATCCTTCTATGAGCA
TTCATTTTTGGACCAAGCCTGGATTTACAATTCTATTACTGGCCCAGACTTCATTT
CTATCCAATTTCATTCCACTGTGCTATAGTTTACAACATATAATTTGACTTATAAA
TAATTCCTGACTATGGGTTTAAAGACTGAAAATGGATCAATAGAAACTTTGAAAAT
GTTAACATCTTGATTGCTTTTCTCAGTGTAGAAATGGACAATGTTTAGCTTAAAAA
CTGCATGTTTTTAATGAGATACGGGGTTGAAAGACTTATTCCTGGAATTTATTGTT
CTGGAGAAAGCCTGTTGCTATCTGCCATACCTTGGTTTACTTTGTGCAAAATGAGC
TTCTTTTTAAGTAATGAGCTCTTTCCATGTTCAGCTTAAATTGCTGTCTTAGACAC
TTCATCAGGGTTCCCTGCTCTGCCTCATTCCCCCTTTTGCTCACTTGCAGCCTTTG

ACATAATCCTGGGAGGCAATTGGCATCATACATATTTTGCTTTGTAATCTCCTGCT
TTGATTCTGACTGGGACCCAGC

Sequence ID - 453 nt: 747
GGATCTAAGACCAGCCTGGCAGCCACCAGATGGTGATTCTAGTCCTGGCTCAGTCA
GTAATAGGTCACTGACCCCAGAGAAATCAATTCAGCCTCCCCAGGTCCTTGGATTT
CTTTCTGTGAAAATGAAAGCATAGGTAGGAATTTCCCATGGAACAGCTAGCAGAGG
AGAAATATTAAAAGTCAGGAGACTCATGCTATAGTTTTCATACTTCATTACAACAA
TGTTGTTTAGGACAAGTGAGTTAACCTGTTAGCTTCCTCTATATAAAATGGAAAGT
CATTAAAAACCTACATAGCAGGGTTCTTGTGAAGATCAAGTGATAATGTAGGAAGC
ATGTACAAATGTCACATTCTGCCGTCACGTAATGGTCCTCACAGCTTGAGGTAGCA
TTTAGCATGTGTCATGATTTAGTACAAGGGTTGGCAAACTGTTGCTCTTGGATTAA
GTCTGGCTCATTGCCTGTTTTTCAAAGAAAAAAATTGTATATGTGTGTATATATGT
TATATATAGGTACACACACATATGTGCTATATATAGCATATATACACACATAATAT
ATAAACATGTACATATATAGCATTATATATATACCGTGTATAATATCTCCAGTCCT
CATGACCAGCCATGCTTGTTCATTTACATTTGCATACTCTATGATTGCTTTCATGC
AACAATGGCAGAGTTGAGTGATTGTTTTGCACAGANACTGTATGGCCCACTAAACC
TAAAATATTAATCTCTGCC

Sequence ID 454
CTCCTGCCGGGCTCGTGGCGGCTTCTGTCCGCTCCGCGGAGGGAAGCGCCTTCCCC
ACAGGACATCAATGCAAGCTTGAATAAGAAAAACAAATTCTTCCTCCTAAGCCATG
GCATATCAGTTATACAGAAATACTACTTTGGGAAACAGTCTTCAGGAGAGCCTAGA
TGAGCTCATACAGTCTCAACAGATCACCCCCCAACTTGCCCTTCAAGTTCTACTTC
AGTTTGATAAGGCTATAAATGCAGCACTGGCTCAGAGGGTCAGGAACAGAGTCAAT
TTCAGGGGCTCTCTAAATACGTACAGATTCTGCGATAATGTGTGGACTTTTGTACT
GAATGATGTTGAATTCAGAGAGGTGACAGAACTTATTAAAGTGGATAAAGTGAAAA
TTGTAGCCTGTGATGGTAAAAATACTGGCTCCAATACTACAGAATGAATAGAAAAA
ATATGACTTTTTTACACCATCTTCTGTTATTCATTGCTTTTGAAGAGAAGCATAGA
AGAGACTTTTTATTTATT

Sequence ID - 458 nt: 682
TGCCACTGAAGATCCTGGTGTCGCCATGGGCCGCCGCCCCGCCCGTTGTTACCGGT
ATTGTAAGAACAAGCCGTACCCAAAGTCTCGCTTCTGCCGAGGTGTCCCTGATGCC
AAGATTCGCATTTTTGACCTGGGGCGGAAAAAGGCAAAAGTGGATGAGTTTCCGCT
TTGTGGCCACATGGTGTCAGATGAATATGAGCAGCTGTCCTCTGAAGCCCTGGAGG
CTGCCCGAATTTGTGCCAATAAGTACATGGTAAAAAGTTGTGGCAAAGATGGCTTC

CATATCCGGGTGCGGCTCCACCCCTTCCACGTCATCCGCATCAACAAGATGTTGTC
CTGTGCTGGGGCTGACAGGCTCCAAACAGGCATGCGAGGTGCCTTTGGAAAGCCCC
AGGGCACTGTGGCCAGGGTTCACATTGGCCAAGTTATCATGTCCATCCGCACCAAG
CTGCAGAACAAGGAGCATGTGATTGAGGCCCTGCGCAGGGCCAAGTTCAAGTTTCT
GGCCGCAGAAGATCCACATCTCAAAGAAGTGGGGCTTCACCAAGTTCAATGCTGAT
GAATTTGAAGACATGGTGGCTGAAAAGCGGCTCATCCCANATGGCTGTGGGGTCAA
GTACATCCCCAATCGTGGCCCTCTGGACAAGTGGCGGCCCTGCACTCATGAAGGCT
TTCAATGTGC

Sequence ID 459
TCCCGGAATCGCGGCCGCGTCGACCTTGTCCTTGAGCGTCAACCTTCTTTCCCTGA
AGTGGCTGGGGTTCCTGTTTCCTTCTTTGATTGACAACTTGTGTTAACCCTCGCAC
ATCTCTGGGCCAATTTTTGCTTGTAAGTCTTTCCGGAGACCCCTGGAATTTAAATC
ATTAGCACCGCGCCCTTCCCCGAAGAGTCTTCGAAGGGTTGCCGCTTTTCGGTGGC
GCAGTTCTCGCGAGAAGGTGACTTTCTTTCTCGGTATTTCCTGGTTTCCAGAATCC
TTAGCGCGAGGCGGAAAAAATATTTCTCCCAGCTTGTGTTGATGCCGCGATTTTGA
CTGAGACTTCTTCCCACGATTTCTGTTTTTGCTTCTCCAAGGAAAATGGCAGCTCC
CGAGCAGCCGCTTGCGATATCAAGGGGATGCACGAGCTCCTCCTCGCTTTCCCCGC
CTCGGGGCGACCGAACCCTTCTGGTCAGGCACCTGCCGGCTGAGCTTACTGCTGAG
GAGAAAGAGGACTTGCTGAAGTACTTCGGGGCTCAGTCTGTGCGGGTCCTGTCAGA
TAAGGGGCGACTGAAACATACAGCTTTTGCCACATTCCCTAATGAAAAAGCAGCTN
TAAAGGCATTGACAAACTNCATCAACTGAAACTTTTAGTCATACTTTAATCG

Sequence ID - 460 nt: 536
CAGAGATCAAAATAGGCCTTACACAGTGCGACGCGAATTTAAAAGATTACCCCATT
CAGGTGTATGGATTTTGCAGTATTAAAGATGCTGCCTGGAATAGGTCATTATCTTC
TCCAAGTACTCTGTTAAGTCAATGAGTCACATAGAGTATAAGGTTTATTATCTGCT
TTTCTTTCATTAAATAAATCTTTATTGAATTTCTACTACATTAAAAAACCAAACCA
AAACAAAACAAACAAAAAAAACACTTCCCTGAGCCATAAAGGAGAAGGTAGTTTTG
ACTGGAACCTTGAAGGATGGGTAAACTTTCAGCAGATAAAGATTGAGAGAAGACCT
TCCAGGTAGAGAAAGCAGTGTGGGCACAGGCAAAGATGGAAGAACACACGTGGCTG
TGGGAAACACAGCTAGAAGCCAGTGCGGATAGAGAGTAGGCTATGATGTGCAAAGG
TTANACACTGGGAGAGACAGGTCCATGAGAGTAGCTTGGACTAACACAGGGAGGGT
TTGGAATCCCAACTGGGGAACCTANAAATCAA

Sequence ID 461
TAGGAGGCTTATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCT

ACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCA
CAACACTTTCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGC
ATACACCACATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAG
TAATATTAATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTA
ATAGTAGAAGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCACCCTA
CCACACATTCGAAGAACCCGTATACATAAAAT

Sequence ID 462
TCTTTATCAAGTTGAGAAAGTTCCTCCCCTCTATTCCTAGTTTGCTAAGAGTCCTT
CTATCCTATTTCTTAATGGTTTAGTAGATGACTCTGTGGTACTTTGAAGGTTGTTT
GCAGAATTTCCATGCCATAGGCAATTTACCTTTCCTTGACATTTGAAGGATTGATG
TTGGTGCCAAGTATAGAATCTTCACAGAGTCCTCCTGTAGCTTCTAAAGGTTTAGC
TTGAAAATGTTAATTGCTTAACGCTAGTAAGTGAGTGAAAAAGCTGGGGATAAATT
TTGTATCTTGCTTATATTTCAGTTCCCACCTCTGTCCNGACNAAACCCCCATATAT
AA

Sequence ID 463
TAGTTTACATATCCCAACCTTTAAAAATATTCCTCTTATTAGCTTTATATTCACTT
TATAGAAGTTGAGTTTTAATTAAAATTCTTGGCATCCTGAAGTATGTCACATAGCA
TGTGCTCCTTATAAATATGTTGATATCTCAGAAGACAGCATCCCGGTTTTCATTTT
ATAAAGTACCATACTTAAGAATGCTGTAATACTTATCTTTTATAACATGTTTCCTT
CGCTTTGCTTGNCTTTTATGNCATCAGTTTTAACTGTTTACTTCATTTAACAGNTT
ACATCATNCAACAGTTTACTTCATTAAACAGTAGGTGGAAAAATAGATGCCAGTCT
ATGAAAATCTTCCCATCTATATCAAAATACTTTCAAGGATATACTTT

Sequence ID - 464 nt: 615
CGACTTTCAACCATCAAGTGAGGAATACCTTCACATAACTGAGCCTCCCTCTTTAT
CTCCTGACACAAAATTAGAACCTTCAGAAGATGATGGTAAACCTGAGTTATTAGAA
GAAATGGAAGCTTCTCCCACAGAACTTATTGCTGTGGAAGGAACTGAGATTCTCCA
AGATTTCCAAAACAAAACCTATGGTCAAGTTTCTGGAGAAGCAATCAAGATGTTTC
CCACCATTAAAACACCTGAGGCTGGAACTGTTATTACAACTGCCGATGAAATTGAA
TTAGAAGGTGCTACACAGTGGCCACACTCTACTTCTGCTTCTGCCACCTATGGGGT
CGAGGCAGGTGTGGTGCCTTGGCTAAGTCCACAGACTTCTGAGAGGCCCACGCTTT
CTTCTTCTCCAGAAATAAACCCTGAAACTCAAGCAGCTTTAATCAGAGGGCAGGAT
TCCACGATAGCAGCATCAGAACAGCAAGTGGCAGCGAGAATTCTTGATTCCAATGA
TCAGGCAACAGTAAACCCTGTGGAATTTAATACTGAGGGTGCAACACCCCATTTTC
CCTTCTGGAGACTTCTAATGAAACANATTTCCTGATTGGCATTAATGAANAGTCA

Sequence ID 469
GATTTTTAAAAATACATATAGCAAAAATATTACAGGGTCAGGGGAGACAATTAGAA
TGATATAATTCAAAGTGGATTAAAAAAAAAACTGTCACCCAGAATACAATACCCAG
CAAAGTTGTCCTTCATAAATGAAAGAAAAATNAAATCTTTNCCNAACNA

Sequence ID 471
TCCCGGGAATCTGCAGGATCCGTCGACT

Sequence ID 472
GACAGTGCCCAGGGCTCTGATATGTCTNTCACANCTTGNAAAGTGTGAGACAGCTG
CCTTGTGTGGGACTGAAAGGCAAGATTTGTTCCTGCCCTTCCCTTTGTGACTTGAA
GAACCCTGACTTTGTTTCTGCAAAGGCACCTGCATGTGTCTGTGTTCTTGTAGGCA
TAATGTGAGGAGGTGGGGANACCACCCCACCCCCATGTCCACCATGACCCTCTTNC
CACNCTNACCTGTGCTCCCTCCCCAATCATNTTT

Sequence ID - 473 nt: 694
TGGGCTTTGGGCTGGCTGCAGTCTGTCTGAGGGCGGCCGAAGTGGCTGGCTCATTT
AAGATGAGGCTTCTGCTGCTTCTCCTAGNGGCGGCGTCTGCGATGGTCCGGAGCGA
GGCCTCGGCCAATCTGGGCGGCGTGCCCAGCAAGAGATTAAAGATGCAGTACGCCA
CGGGGCCGCTGCTCAAGTTCCAGATTTGTGTTTCCTGAGGTTATAGGCGGGTGTTT
GAGGAGTACATGCGGGTTATTAGCCAGCGGTACCCAGACATCCGCATTGAAGGAGA
GAATTACCTCCCTCAACCAATATATAGACACATAGCATCTTTCCTGTCAGTCTTCA
AACTAGTATTAATAGGCTTAATAATTGTTGGCAAGGATCCTTTTGCTTTCTTTGGC
ATGCAAGCTCCTAGCATCTGGCAGTGGGGCCAAGAAAATAAGGTTTATGCATGTAT
GATGGTTTTCTTCTTGAGCAACATGATTGAGAACCAGTGTATGTCAACAGGTGCAT
TTGAGATAACTTTAAATGATGTACCTGTGTGGTCTAAGCTGGAATCTGGTCACCTT
CCATCCATGCAACAACTTGTTCAAATTCTTGACAATGAAATGAAACTCAATGTGCA
TATGGGATTCAATCCCCACCATCGATCATAGCACCCCCTATCAGCACTGNAAACTC
TTTTGCATTAAGGGATCATTGC

Sequence ID 474
GGCAGCGCGGGGAGCCCGTCGGCGCCGGCGGGCGGGCCGGTTTCGAAGTTGATGCA
ATCGGTTTAAACATGGCTGAACGCGTGTGTACACGGGACTGACGCAACCCACGTGT
AACTGTCAGCCGGGCCCTGAGTAATCGCTTAAAGATGTTCCTACGGGCTTGTTGCT
GTTGATGTTTTGTTTTGTTTTGTTTTTTGGTCTTTTTTTGTATTATAAAAAATAAT
CTATTTCTATGAGAAAAGAGGCGTCTGTATATTTTGGGAATCTTTTCCGTTTCAAG
CATTAAGAACACTTTTAATAAACTTTTTTTTGATAATGGTTAAAAAAAAAAAAAAA

A

Sequence ID 475
CATAATAAAAAACAATCAACAAACAGGGAATGGAAAGAAACTTCCTCAGCATGGTG
AAGGCCACATATGAAAATCCCACAGCTAACATCATACTCAATGATGAAAGACTGAA
AGCTTTTCTCCTGAGATCAGGAACAAGACAAAGATGTCACCTTTTGTCACTTCTAT
TCAACTCATTATTGGAAGTTTTTGCCAGAGCAATTAGGTAAG

Sequence ID - 476 nt: 476
CAGAATCTTTTCATAGGCTGAATGTTGCTCCACAATGTGTCCTTTGACTATCTCTG
GCTAATTATTATTTTAATCTCTTCTCAGCTTTTCCAAGAACATAACGTTAACCAAA
GATCTTAGGCCATTCACAACTCTTTTGTAAAAATTAATGTGGATGTGAAACGAGGC
AACAAATCCTGAAGTAGAAAGTTATTCCTGGCCAGGCACGGTGGCTCACGCCTGTA
ATCCTGGCACTTTGGGAGGCCGAGGTGGGTGGATCATGAGGACAGGAGATCGAGAC
CATCCTGGCCAACATGATGAAACCCCATCTCTACTAAAATACAAAAAATTAGCTGG
GCATGGTGACGCGTGCCTGTAGTCCCAGTTACTCGGGAGGCTGAGGCAGGGGAATT
GCTTGAACCTCGGAGGTGGGAGGTTGCAGTGTGCCGAGATCACGCTACTGCACTCC
AGCCTGGCAACAGAGCAAGACTCCATCT

Sequence ID 477
AAACAGAAAGTTTCTTCTAAAGGCATGATTCAGTTAAGTCATTCTTAAGTGTTAAA
AAATTGTGAAAAATGTGCCTGTAATCCCAACACTTTGGGAGGCCGAGGCAGGCAGA
TCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACAAGGTGAAACCCCGTCTCTA
CGAAAAATACCAAAAACATTAGCCGGGCGTGGTTGTGGGCGCCTGTAGTCCCAGCT
ACTTGAGAGGCTGAGGCAGGAGAATG

Sequence ID 478
TTCTTGGGATATTGATGACTACTGTCTGAGAGGTGCTGTGGGGAGATTTTCAGGAT
TGTGTGGTCTTTGAGGGGGGTGTTTTTTAAGACAACATTGACCACTGTCCACTGT
CCACATGATCATTGTAAAATTGCAATGCCGCATGCTAGTTGGTTACATAAGACATA
ATTCCAGTGATTGAAGGTGGTTACACTGTATGGTGGTGTGTTCAAGATGGCACTGG
CATCTTTGAGCAGAGCCTGGCTATGCAGCATCATTTGAGTTTTTTAAACACCCTAN
AGGTCTGGTTGTTGTTGCTGTTGTCCTTTCCTGTGAAAGTCACAANANAAGTTACA
GTCCAGGTGAACCTGGAGTTTATAGGTTGGTTTTGTTTCTGNTATATATATATATA
TATATATTTTTTTTTTTTTTTAACATTTACCTGTAGTGCTGTAGCTGTTGATACTA
TCACCTGCATGCTATTTCTAGTGAGTGCTAAATACAGTATGGTCCAATGACAATAA

CAGCCCATGGTACTGCCAG

Sequence ID 479

CATCAGTCTGTTATCCATGCTGACTTTCCGAAGACTTGCAGCTACTGCATTGATAT
CTTTCCTGCCAATAAGCAAAGTGTTGAACACTTCACAAAATATTTTACTGAGGCAG
GCTTGAAAGAGCTTTCAGAATATGTTCGGAATCAGCAAACCATCGGAGCTCGTAAG
GAGCTCCAGAAAGAACTTCAAGAACAGATGTCCCGTGGTGATCCATTTAAGGATAT
AATTTTATATGTCAAGGAGGAGATGAAAAAAAACAACATCCCAGAGCCAGTTGTCA
TCGGAATAGTCTGGTCAAGTGTAATGAGCACTGTGGAATGGAACAAAAAAGAGGAG
CTTGTAGCAGAGCAAGCCATCAAGCACTTGAAGCAATACAGCCCTCTACTTGCTGC
CTTTACTACTCAAGGTCAGTCTGAGCTGACTCTGTTACTGAAGATTAGGGAGTATT
GCTATGACAACATTCATTTCATGAAAGCCTTCCANAAAA

Sequence ID 481

CACACTTTCATGATAAAAACAGAACCTAGGAATGAAAAGAAATTATAGCAACATAA
TAAAGACCATATATGAGAAGCCCACAGCTAACATACTGTATGGTGAAAAACTGAAA
GCTCTTCCTCTAAGATCAGGAACAAGGCAAGGATGCCCATTCTTGCCACTTCTATC
GAACGTAGTACTGGAAGCCCTAGCCAGAACAACTAGGCAATAGAAAGAAATTAAAG
GCATCCATNTCAGAAAGGAAGAANCAAAATGCTGTCTGTTTAANATGACA

Sequence ID 482

TTTCTATANAAAAAAATTTTTTAAAATAATTGTAAAGTTAGATTTAAAATTGTAAA
ATATAAAATCACAAAGGAATGTACCCAATAAAATGTAAATGCNCCATAAAAAAAAA
AAAAAAAAAAAAAAAAAA

Sequence ID 483

CGNTAACGTGCAATCCGCCGCACGCCAGCAAACTGGACAAACTCCGGGATCTCATC
GAAGCGATTGAGCACCAGTACCAGAGTAATACCGGACTGATGTAACGAGGCGAGTC
GCTCATCCAGCTTGCTGACGTGAGGCAACATCCAGGCCATCGAACGGNTCATCAAG
AATCAACAAGTCAGGCTCCGACATCAGCGCCTGACACAGCAGGGTTTTTCGCGTCT
CGCCAGTGGAAAGGTATTTAAAGCGTCNGTCGAGGAGGGCGGTAATACCGAACTGC
TGCGCCAGTTGCATGCAACGCGGTGCATCCTTTACTTCATCCTGAATGATCTCAGC
CGTAGTGCGTCCGGTGCCATCTTCGCCAGGGCCGAGCATATCGGTGTTATTCCGCT
GCCATTCGTCGCTGACGAGTTTTTGCAATTGCTCGAAGGAGAGACGAGTGATGTGG
GAAAACTGGCTTTGCCGTTCACCTTTCAAAAGCGGGAAGTTCCCCCGCCAGCGCGC
GGGCCAGGGCCCGAT

Sequence ID 484
TTTTTTTTTTTTATTCTATTAAAAAATGTTNNTGAAAAAAGATACTTAAATTTTAA
AGATAACTNAATTCCTAANGATTTAAAATAATCCAAGCAGAGATGAAAGANCAAAT
GCAAATGCNTAAAAAGACCCCANAGCATTGTTAGCAAAAAGCAAATATAGTTAGCC
AAGCATATATATNTCATAAAAGCAATAANAAGGCNTAAAGCAAGTTTGGGGAGAGC
TTATTTAAAACTTGTAAAAATCATTTGAATTTTTAAAAGTTTTCAAAC

Sequence ID - 485 nt: 551
TTTGGAACACAAAGTTCCCTTTTTAGAAGAATAGGTATTGAGCCCTTGAGCGTGGG
TAGAAAGATAGAGACAGAGTGATTTGCAAAATAATGGAGGATCATATTTATATATG
AATTTTCACTTATTTGAACTTTCAGATATCANCTTNAAAANCTTTGGTTTAAGTAA
AGTNTNTTAATGAGACTCCTTGGATGAAAGTAACCAAAACCAGTAAAAATAAGGTA
ATAAGGATGTAATAGTTTCTTATGGACACTCAACAGCTAGAATGCAGTTAGTCTCA
GAAAAGAATTAGAACAAATAACTGGAAGGCCATCAGGAGTCCAAAACCATCACTCT
TTTATATTTTATATTTTATTTTTCTCTCTTCANATGAGCATTCTCTTTCTATGTCC
ATATGGTANAAGGCGGCAGCTCCATAGATTATGGCTTCAGATGTTACAGTTCCGCT
NAATGCAGGGACAGACTTGCTATCTTTCAGTCCCCTTACATATCCTGGGGAGAGAG
CAAATGATTGACTGGCTTGAGTCAGGTGCCCGTTCCCTTTCCAATCT

Sequence ID - 487 nt:224
GTTTGNTTGTGACCATCTGTACTTGTAATTTCTTTACNTTCATTGGTATGAAAAAT
ATGTTCTTAGAAGCANGAAAAAGAATTCAGNTTTGCTTTGTATACTAAATTAAATG
CTGTAATTTTGATAAAATGAAAAATCTGCTTTATTTGCAACAATTGGTTTCTTCCT
TGACGTCAGCCTCACTCTTGGACTTTGGTATTCAGCCNGNCACCCCTGGGAATTCC

Sequence ID - 488 nt: 349
GTGCCTCCCTGTGTGAGTAGCCTAAGGTGCATTGAAAAAGACTGGGATGTGTTTTA
TTTTTTTGTATTAGATAGCATTAACCTTACTGTTGAAGTATTTTTGGTGGAGTATT
AGTGACAAGCCATTGAGTCTTAAGCCTTACGGCTTCCTATAAAATCACTAATTTCG
TGTGTGTTTGTGTGTAGGTTACGTTATATATAGGATTCGTGTTCGCCGTGGTGGCC
GAAAACGCCCAGTTCCTAAGGGTGCAACTTACGGCAAGCCTGTCCATCATGGTGTT
AACCAGCTAAAGTTTGCTCGAAGCCTTCAGTCCGTTGCAGAGGANCGAGCTGGACN
CCCTGGGGGGCTC

Sequence ID 489
TTAACAGCTGCATAGAGTTTTAAAAGTACATTATATTTTGTCAGACAAGTAAAATA
TCTGTTTTTCACGCAAAAAAAGCCATGAAATACGTAATTTTTTAAAGACAAAAAAT

CATCTTTTGAGTTTGCTCTTTGGTTTTTCTTCATTCCTTTTGAGGATTGGGAAAAC
AGAAAGATTCTTTGATTTGGGTAATGAAGAGGTAATTTGGGACAGTGTGGTGGTAC
CAGGAAGAAAGAGGATTGGAAAGGCCAGTACTGTTTTAGTTGCTCGGCACTGTTGG
TTTTGTTTTAATGTGGTTGCCCTGTCCACTACATGGTTCTATCAGTAGTGTAATCC
ATTTTCAATGTAAAGCTCTTTTAGTTTTTGTCATAGACATAAATTAATATTTTGAG
AGGCATCCCTCACCTGTTCATTTCTTCTGTGTTGAAATGAAGTACTTAAAATTACC
GTTATACATGAACTTTGTGGACTGTAAGATTTGTTATATATGTTCAAATGCCTTTT
AGCTGGCTTTTTAATTAATATGCCTGTTTGAGTGCTTAATACAATGTAATGNGGA
TTGTAAATCATACCTATTTTAAATCATTCCTTCCTGTATATTTGNACTCAGAGAGC
CTTATTTTATTCTTCCAGC

Sequence ID - 491 nt: 382
TTTTCTTAGAACTTTATTTTTTCTGGCCAGGCGCAGTGGCTCACACCTGTAATCCC
AGCACTTTGGGAGGCCAAGGCAGGTCGATCACCTGAGGTCAGGAGCTCAAGACCAG
CCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCG
TGGTGGCGCATGCCTGTAATCCCANCTACTCAGGAGGCTGAGGCAGGAGAATTGTT
TGAACCCGGGAGGCGGAGGTTGCANTGAGCCGAGATTGCGCCACTGCACTCCAGCC
TGGGCAACAGAGCGAAACTCCATCTCAAAAAAAAAAAAAAAAAAACAACCTTTATTT
TTTCTGATTTTAAAAGTAATAACTAGTTTGTAGAAACATTAAAAGT

Sequence ID 492
ACCCTAAACATAACTTAAAATTTGTTNGGAATTTGAAAGTACAGAATTTTCCTGTA
ATTGAGACTNTTTAAACTTTTGTGGTTGGAGAAGGTATTCTATTTTTTGAAAATAT
CTGTAAGTTTTATCTAAATAGTAAACTCTAAGTATTCTTCCCCTTTACTTACAGCC
ACCCTGGGAATCTGAGACTAGAGAAAATAAAGTTTGTCTCTTGTTCTAAGGAGGGT
CTGGTTTAGAAATCTGATTTAGACATAGAAAAATTGCAAGAAGCTTGAGGTGATTG
GAAGATACGATTTTGTTATCAAAGNATGTTTCTGTTTTATAGATTTTATTCATCTA
CAACTCCTTATTAATATATTTAAGAAGTCATTAACCCACCATTGATTACTTGATAT
AAAAGGAGAANCGGTGGTAAAAGGTGAAATANAATTTTTAATTTTTTTTTTTTTAA
GTTTAGGATTTTTTTTTAAATTCTAAGAGTTTCTGTCATTTGGGGACAATCAGAA

Sequence ID 493
TGGGAATCATAATTNGTTAACTGAAGCTNATAAGATGAGAGCATTCANAGAGAAAA
GAACGGAAAGATTGAATATCAGTTTCCCTTCTTTAAAAAAATTGTGGATATGTGAT
CTAGCTTCTTGAGCATCACAGTGACTGATTGGCTCGTGGTAATTGATCGCTATGCT
GACAATCTTATCTCCACCTATGTCATTCAATTTTCTAAGAGGCAAAATCCTTAATC
AGGAGGAGAGTTTAGCTCTAGCTAAATTTCCCTTGTCCAGCATGCTCCTGCTCCCC

CAACTTGTGGAAACAGCTAAAGGATTGGACTAGGAGCANAAGTTTGGAATGGTTAA
AATGTAGCAACATGTGTTTCCTGAAACAAAATTCCACTATAATAAAAAAAGCATTT
GAATGCTCCCTTGTAATTCTGTTGGAGCTTGTTGCCTTTTTTATGACACAACCATA
ATCAGTGATAGACAGTAGCATAAAGAAGCAAGAGCAAAGCAATTAAGTAATAATAG
CACTACAAAAATGTGTGCTGTACTTACCAAACACGACATTTATGAATTATTANATA
GGAATAAGGGGATGGT

Sequence ID 494

GACCCAGCCATCTAAATAAGTTRTACATGTTGCGTATTTTTTTGTTAGGGACTTAT
CTTCCGAAGAGGAAAGGTTTATGAAACCTAAAGTAACAATGATAGCTTGGAATCAA
AATGATAGCATTGTTGGCACAGCTGTGAATGATCATGTCCTCAAAGTGTGGAATTC
TTACACTGGACAACTGCTTCATAACTTAATGGGACATGCTGATGAAGTATTTGTTC
TGGAGACACATCCCTTTGATTCCAGAATTATGTTATCTGCAGGACATGATGGCAGC
ATATTTATATGGGATATTACAAAAGGTACCAAGATGAAACATTATTTTAATATGGT
AAGTGAAGTGAGATGTACCTTGATACATGCTTGATAATTTGTTTAGAGTATTTGGG
TTATGCGGCTTACCCAGAAATTGATCTGCTTGTTTTGGCAGTTTGTTTTTACAAAT
CAACATATTCAAAGCCTGCTAAATATTAGACAGCTACATGTATATACGTACATACA
TGAA

Sequence ID 495
TTTC

Sequence ID 496
CTCGCTGGCGGGAGGCCACGGGCTTTCCACAGCGCGGGGGAACGGGAGGCTGCAGG
ATGGTCAAGCTGACGGCGGAGCTGATCGAGCAGGCGGCGCAGTACACCAACGCGGT
GCGCGACCGGGAGCTGGACCTCCGGGGGTGATCTGGACCCTCTGGCATCTCTCAAA
TCGCTGACTTACCTAAGTATCCTAAGAAATCCGGTAACCAATAAGAAGCATTACAG
ATTGTATGTGATTTATAAAGTTCCGCAAGTCATAGTACTGGATTTCCAGAAAGTGA
AACTAAAATTTTAATCCAGGTGCTGGTTTGCCAACTGACAAAAAGAAAGGTGGGCC
ATCTCCAGGGGATGTAAAAGCAATCAAGAATGCCATAGCAAATGCTTNAACTCTGG
CTGAAGTGGANAGGCTGAANGGGTTGCTGCAGTCTGGTC

Sequence ID 497
GAAGACCTCACATCTGAGAGCTCATCTGCGTTGGCATTCTGGAGAACGCCCTTTTG
TTTGTAACTGGATGTACTGTGGTAAAAGATTTACTCGAAGTGATGAATTACAGAGG
CACAGAAGAACACATACAGGTGAGAAGAAATTTGTTTGTCCAGAATGTTCAAAACG

CTTTATGANAAGTGACCACCTTGCCAAACATATTAAAACACACCAGAATAAAAAG
GTATTCACTCTANCAGTACAGTGCTGGCATCTGTGGAAGCTGCGCGAGATGATACT
TTGATTACTGCAGGAGGAACAACGCTTATCCTTGCAAATATTCAACAAGGTTCTGT
TTCAGGGATAGGAACTGTTAATACTTCCGCCACCAGCAATCAAGATATCCTTACCA
ACACTGAAATACCTTTACAGCTTGTCACAGTTTCTGGAAATGAGACAATGGGAGTA
AATATTACACAAATACTTATTCATTGNGGTTATTTTTATACAGTAGTGAGAAGAAT
ATTGTTCCTAAGTTCTTAGATATCTTTTTTTGGATGTGCAAAAATTTTTGGATTGA
CAGTAACTTGGGTATACATGACACTGAAATGCCTTACTTTGGATGA

Sequence ID 499
TGCCTGCGGGCCAGGACCTCGCCCAGCCCATGTTCATCCAGTCAGCCAACCAGCCC
TCCGANGGGCAGGCCCCCCAGGTGACCGGCGACTGAGGGCCTGAGCTGGCAAGGCC
AAGGACACCCAACACAATTTTTGCCATACAGCCCCAGGCAATGGGCACAGCCTTCC
TCCCCANAGGACCCGGCCGACCTCAGCGCCTCCTGCAGGCTAGGACACTGGTGCAC
TACACCCCATGCCTGGGGGCCGAGATTCTCCAGCAGAAAGATGCAATATTTTTTGT
TTCCTTTTTTTCCATTTTTTTCTCTAAGGAATCAATATTTCAATATGTTGAGTGTG
TGTCCAATGCTATGAAATTAAAATATTAAATAACATATTTATGGCATTTTCTTGAA
GAGTGTGGTTGAAGAAATATTTCTCCTTTTGTTTTTCTTTTTTTTTTGNTTGNTAC
TGCCACTTCTTTTTAGGAGCAAATCTCCCCAGGGGTGTACGGNATTTCTTGACTCT
GGGAACAGCTGCTACCCCCAAGACTTGCCACGTTGTTCTGCCCTCAAATGGAATTA
AGTG

Sequence ID - 500 nt: 390
GGAATATGGTCAGGATCTTCTCCATACTGTCTTCAAGAATGGCAAGGTGACAAAAA
GCTATTCATTTGATGAAATAAGAAAAAATGCACAGCTGAATATTGAACTGGAAGCA
GCACATCATTAGGCTTTATGACTGGGTGTGTGTTGTGTGTATGTAATACATAATGT
TTATTGTACANATGTGTGGGGTTTGTGTTTTATGATACATTACAGCCAAATTATTT
GTTGGTTNATGGACATACTGCCCTTTCATTTTTTTCTTTTCCAGTGTTTAGGTGAT
CTCAAATTAAGAAATGCATTTAACCATGTAAAANATGANTGCTAAAGTCAGCTTTT
TAGGGCCCTTTGCCAATAGGTANTCATTCAATCTGGTATTGATCTTTTCACAAA

Sequence ID 502
ACCCGCCATCTTCCAGTAATTCGCCAAAATGACGAACACAAAGGGAAAGAGGAGAG
GCACCCGATATATGTTCTCTAGGCCTTTTANAAAACATGGAGTTGTTCCTTTGGCC
ACATATATGCGAATCTATAAGAAAGGTGATATTGTAGACATCAAGGGAATGGGTAC
TGTTCAAAAAGGAATGCCCCACAAGTGTTACCATGGCAAAACTGGAAGAGTCTACA
ATGTTACCCAGCATGCTGTTGGCATTGTTGTAAACAAACAAGTTAAGGGCAAGATT

CTTGCCAAGAGAATTAATGTGCGTATTGAGCACATTAAGCACTCTAAGAGCCGAGA
TAGCTTCCTGAAACGTGTGAAGGAAAATGATCAGAAAAAGAAAGAAGCCAAAGAGA
AAGGTACCTGGGTTCAACTAAAGCGCCAGCCTGCTCCACCCAGAGAAGCACACTTT
GTGAGAACCAATGGGAAGGAGCCTGAGCTGCTGGAACCTATTCCCTATGAATTCAT
GGCATAATAGGTGTTAAAAAAAAAAAAATAAAGGACCTCTGGG

Sequence ID - 503 nt: 109
ACATTTTCCGGNCCTTTTGCCATACACAGTTACAGAGATCAGTCAAATCCATACCA
CCACTGAGATCTCATTTATTGCCACAGATGCACAAAATAAATAACCCAAAATC

Sequence ID - 504 nt: 374
CCAGCAACGACCCATACCTCAGACCCGACGGCCCGGAGCGGAGCGCGCCCTGCCCT
GGCGCAGCCAGAGCCGCCGGGTGCCCGCTGCAGTTTCTTGGGACATAGGAGCGCAA
AGAAGCTACAGCCTGGACTTACCACCACTAAACTGCGAGAGAAGCTAAACGTGTTT
ATTTTCCCTTAAATTATTTTTGTAATGGTAGCTTTTTCTACATCTTACTCCTGTTG
ATGCAGCTAAGGTACATTTGTAAAAAGAAAAAAAACCAGACTTTTCANACAAACCC
TTTGTATTGTANATAAGAGGAAAAGACTGAGCATGCTCACTTTTTTATATTAATTT
TTACAGTATTTGTAAGAATAAAGCANCATTTGAAATCG

Sequence ID 505

GTACAGGAGGTAAATTGGATACCCCATCTAAGGGGATCTGTGAGACCAGGTAGTTA
TTTGGAATGAAAGAGTAAGATATTAAACCAGCCAGCATGTCAACAGGTGGGTGATA
GTCTTGTTCTCACAGACAACAGATGGCCATCATCTTAAAACAACATTTATGTTAAC
CAGCAGATAAGGGACTCCTGCATTGTCAGTGGACTTTGAGCCTGAGTTTTTCTACT
TGCATAGGTGAAAGTGGACTGCAATGCTAGTATAAATGCCGTATGATGACTAGTAC
CCCTTAGGGAGCTCCAGTTTGCCTTCCTGGGGAACCACAGACCCCAAGTGTAATTT
CCTGAGGACAGCCCGACTTCT

Sequence ID 506
GTTACTGTGAGCCTGTCAGTAGTGGGTACCAATCTTTTGTGACATATTGTCATGCT
GAGGTGNGACACCTGCTGCACTCATCTGATGTAAAACCATCCCANAGCTGGCGAGA
GGATGGAGCTGGGTGGAAACTGCTTTGCACTATCGTTTGCTTGGTGTTTGTTTTTA
ACGCACAACTTGCTTGTACAGTAAACTGTCTTCTGTACTATTTAACTGTAAAATGG
AATTTTGACTGATTTGTTACAATAATATAACTCTGAGATGTGTGAAAAAAAAAAAA
AAAAAAAAAAAA

Sequence ID - 507 nt: 521

CTGCGGTGGAGCCGCCACCAAAATGCAGATTTTCGTGAAAACCCTTACGGGGAAGACCATCACCCTCGAGGTTGAACCCTCGGATACGATAGAAAATGTAAAGGCCAAGATCCAGGATAAGGAAGGAATTCCTCCTGATCAGCAGAGACTGATCTTTGCTGGCAAGCAGCTGGAAGATGGACGTACTTTGTCTGACTACAATATTCAAAAGGAGTCTACTCTTCATCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCACAAGAGAAAGAAGGTTAAGCTGGCTGTCCTGAAATATTATAAGGTGGATGAGAATGGCAAAATTAGTCGCCTTCGTCGAGAGTGCCCTTCTGATGAATGTGGTGCTGGGGTGTTTATGGCAAGTCACTTTGACAGACATTATTGTGGCAAATGTTGTCTGACTTACTGTTTCAACAAACCAGAAGACAAGTAACTGTATGAGTTAATAAAAGACATGAACT

Sequence ID 508

AAGCTCATGATTTTAAATGTATTTTTCTAATAAACTATACTCCCATTTAAAAATCACCAATACCTTAATGTTTCAATTATATAAGCTAATTAAAAATAAAGGCTGGGCGTGGTGGCTCACTTTGGAAGACCGAGGCAGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGCCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCACATGCCCGTAATCCCAGCTACTGGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGGGGCTGCAGTGAGCCGAGATCATGCCATTGCACTCCAGTCTGGGCAACAATAGTGGAACTCCATCTCAAAAATAATAAAAAAAATAAAATAAAAATAAAATTCAAACCTAAAATAGATGCTCTACTTCAGGAGTGGGCAAATTAATCACCTGCATCCTTTTTTTGGGCTTTC

Sequence ID - 509 nt: 575

TTTTTTTCTAAATGGNGATTACTAATATATGTGGAGACTATTAATCTCTTTTCTGTTGCCATTAGTTCATTTTTCCCCAAAAGCCAATACATGTTCATTACAAAAATGAATTATAAAATATAAGTTAAAAGAAAAACATAAAACCCTACAATCTTACCCACCCAGACAACTACTATTAATACCTTAGTATTAACATATACACATCATGTATATGTATAAATTTATCTTAAACAAAAATAAAATTATTCTTTACATATTGTTTTAAAACCTATTTATCTGGCCAGGTGCCGTGGCTCACGCTTGTAATCCCAGCACTTTGGGAGGCTGAGGCACGTGGATCACCTGAGGTCAGGAATTCGAGACCAGCCCAGCCAACATGGTGAAACCCTGTCTCTAATGGTTTAAATACCAAAAAATTAGCTGGGCATGGTGGCACATGCCTGTAATATCAGCTAACATGGGAGGCTGAGGCAGGAGAATCACTTGAACCANGGAGGGGGAGGTTGCAGTGAGCCGAAATCACACCACTTCACTGCAGCCTGGGCAACAAAGCAAGACTGTCTCAAAAAGAAAAA

Sequence ID 510

CACTGTCATTCCCAGGAGGCTTTGGAGTCAGAACTGGATTCAAATTCTGACTNTAT
GTTGTGTGACTTGGGCCAATAGCTTCTTTNTGTGCCTCAGTTTCTTTAGCTGTAAA
TANACGGGTAGGTCACCCCTTACCCCATAGGTTATGGGGAAAGTTACAGAAAATGG
TCAGCTGGGCNCAGTGGCTCAAGCCTGTGGTCCCAGCNCCTTGGGAGGCCAAGGTG
AGCAGATTGCTTGAGCCCAGGAGTTTGACACCAGTNTGGCAACGTGACGAAACCCT
ATCNCTGTGAAAAATACAAAAAATTAGCCAGGCATGGTGGTGTGTGTCTGTGGTTC
CAGCTGCTTGAGAGTTTGAAGTGGGAGGATCACCTGAGCCCAGAAGGTCGAGGCTG
CAGTGAGCTGTGATCGCGTCACTGCACTCCAGCCTGGC-GACAGAGTGAGA-CCCC
T-TTTGAAAAAAAAAAAAAAAAAAT

Sequence ID 512
GTGAGCGGTGGTGGTTTATTCTTCCGTGGAGTTAAGGGCTCCGTGGACATCTCAGG
TCTTCAGGGTCTTCCATCTGGAACTATATAAAGTTCAGAAAACATGTCTCGAAGAT
ATGACTCCAGGACCACTATATTTTCTCCAGAAGGTCGCTTATACCAAGTTGAATAT
GCCATGGAAGCTATTGGACATGCAGGCACCTGTTTGGGAATTTTAGCAAATGATGG
TGTTTTGCTTGCAGCAGAGAGACNCAACATCCACAAGCTTCTTGATGAAGTCTTTT
TTTCTGAAAAAATTTATAAACTCAATGAGGACATGGCTTGCAGTGTGGCAGGCATA
ACTTCTGATGCTAATGTTCTGACTAATGAACTAAGGCTCATTGCTCAAAGGTATTT
ATTACAGTATCAGGAGCCAATACCTTGTGAGCAGTTGGTTACAGCGCTGTGTGATA
TCAAACAAGCTTATACACAATTTGGAGGAAAACGTCCCTTTGGTGTTTCATTGCTG
TACATTGGCTGGGATAAGCACTATGGCTTTCAGCTCTATCAGAGTGACCCTAGTGG
AAATTCGGGGGATGGGAAGGCCACATGCATTGGAAATAATANCGCTGCAGCTGTGT
CAATGTTGAAACAAG

Sequence ID 513
TTTTTTTTTTATAAACTCCAATCATTTCCAGAGCTACTTAGCTCAGCATCTTTTTT
TTCCACGCTCTTAAGTTGTGTTTATACATTTTTGATACAGTTAGATTGTTTTTGTC
ACATTCTTCATTCTATCCTGGGATCCCCCAACCACCTAAGTGGATTTTTTGATAAT
TTGCATGCTTTAAGGATAACTCTTCATTCTGNAAAGGGCTATGGGTTTTGGCAAAT
GCAGAGTCATGTATCCAAGATTACAATATCGCACAGAAGAGTTTCATCACTATATA
AAACTCACCAGTCTTCCTCCTATTCAACCATCTCCATGCCTTCTTCCCAGCCCTAA
CTCCTTAAAACCACTCATATCTTTACTATTGCTATAGTATTGCCTCTTCCACCATG
TCATATAAATGGAAACATACAGTATTAGTCTTCTCAAACTAGTTTCTTTTACCTAA
CAACATGCATTTAAGATTCATAGTGTCTTTTAATGACTTGATAGATTATTTCTTTG
TAGCTGAATAATATTGCATCTTATAGATGTAACCGTTTGTATATCCATATTTTCTC
ACAGCCTATGACTTGNCTTTTGATTCTCTGAACAGGCCATTCACAAAGCAGAAGTT
TTAATTTTTATAAAGCTAATGNATCAACTT

Sequence ID 515
CCTGGATGACAGCATATCTGTTTATAGCTCAGTTTACTGAATACTTTAAGCCCACT
GTTGAAACCTGCT

Sequence ID - 518 nt: 502
GATGCATGTCCAGCATAGGCAGGATTGCTCGGTGGTGAGAAGGTTAGGTCCGGCTC
AGACTGAATAAGAAGAGATAAAATTTGCCTTAAAACTTACCTGGCAGTGGCTTTGC
TGCACGGTCTGAAACCACCTGTTCCCACCCTCTTGACCGAAATTTCCTTGTGACAC
AGAGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGAGGGAGTATTTCAGGGTTCAC
TTCAGGGGCTCCCAAAGCGACAAGATCGTTAGGGAGAGAGGCCCAGGGTGGGGACT
GGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGGTTCAGGAAGCTTCTGTGCAA
GCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGCCCGCCGCGCTAGCTGTGAGC
TGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCCTGTGGCTTCAGTCCTGCGTC
TGCACCACACATTCAAAAGGATCGTTTTGTTTTGTTTTTAAAGAAAGGTGANAT

Sequence ID 519
CTGCGATNGAGTTTTGAGAGGAAGGANTAAAGTNCTCATCTCNGACGGTGAGAAAG
ATCATNACTAAGGAAACGCAGGGTTGGAAGCAGTGCTGANTGTCCAGTTGAGTTTC
ATGANCAAACATTTGCTGTGGGACCAGTTTTCATGGNGGTTTGTCATTTTGTCCAG
CTGCCTGGAGCTGCTTGGTTGAAGGCACAGAATAATCAGGATTAATTGTTNAACTT
GTATGAATTTCTTTATTTTAAAATAGGAATAATATCTGCCTTGGGAGCAAGTTGTA
AGAGTTAACTGAAAGCTTNAGGAAAAACTTTCCCTTGCTATTTAAGTAGGGCTTTA
CAAGTTACAATTCTATCACAGTTTTAAGATTATAAAC

Sequence ID 521
GCGGCGCANCTGCGGATCCANAAGGNCATAAACGANCNGAACCTGCCCAANNCGTG
TGATATCACCTTCTNAGATCCAGACNACCTCCTCAACTTCAAGCTGGTCATCTGTC
CTGATGAGGGCTTCNACAAGAGTGGGAAGTTTGTCTCAAAAAA

Sequence ID - 523 nt: 585
GATTTACTGTGGGAATTTGCTCATGCAATTATGGAAACCTAGAAGTCCCATAATAT
GCCATCTTCAAGCTGGAATCCCAGGAAAGCAGGTGGTGTAATTCTGAGATTGAAGT
CTTGAGAACCGGGGGAGTCAATGGTGTAACTCCCAATCTAGGGCTTAAGGCCCAAG
GACCAGGGCTGCTGGTGTGCAGATGCAAATCCTGGAGTTCAAAGGATTGAGAACCA
GGAGCTCTGGTGTCTGAGGGCAGTAGAAGATGGATGTTCCAGCTCAAGAAGGGAAA
GTAAGAATCCGTCCTTCCTCCACTTTTTTGTTCTATTCAGATGAGCCCTCAATGGA
CTGAACGATGCTCACCCACACTGTGAGGGCTGGTCTTCTTTATTCAATCCACTGAG

TTAAGTGCTGATCTCTTCTGGAAACACCTTCACAGACACACCCAGAAATAATGTTC
TACCAGCCATGGGCCTGTTACTTAGCCCAGTCAAGTTGACACAGAAAATTAGCTAT
CACAACATCTGTGTGTGTATATACATATGTATTTGCATGTGTGTGTATATATGGNG
TATATATATTCATGTGTGTGTATAT

Sequence ID 524
CTTTTGCCAGTAGGCCCCCTGAGTAGGTTCCTCTATCTTTTGGCATGACCCCAGAA
GTCTTTGATAACTTCCTTGCTTTCTGATGTGACAAGACATCCAGGGCCAGATTGTC
CATATCCTGCCCCGGATGCACGATGCACTGTTTCTCCAAGAATCCCTGTGTCCTTT
GCTGATGATGCCATGATTTTAAGTTCTCTAATATAGTTTTATCTCTTTGTTTCAGA
TAATGCTTTTGTGTTCTCACATGTCCTGCTCTCTCTCTCTCTCATTTTGGTGTT
GATCAGTCTTTCCATAAGATTGTTTATTTCACTAGTCCTTCATTCTTCTTTTTTCT
AAATTTACTCTTCTTGACTAGTATCCTGTCACTTCTGAGGACTCATATTTTTGCAA
CTTGAAAATTATTCTTATTTATTTAAGTATATGTTNCTGAAACTCTCATTAGACAC
ATTTTG

Sequence ID 525
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TCACCTGGTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATGTTTA
ACGGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAAATAG
GGACCTGTATGAATGGCTCCACNAGGGTTCANCTGTCTCTTACTTTTAACCAGTGA
AATTGACCTGCCCGTGAAGAGGCGGGCATAACACAGCTGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAATTTT

Sequence ID - 526 nt: 516
CTTTTCATGGTCTCTTGTTCATTAATCATCTAAAATCCAAGCNCAGAGAATTCAAT
TTTAGATGGTCTCCAGAGCAGAATTTGATGTATAATCTTAATTACAAATCATAGAT
AATTAATATTGNTTACAAAATCANAATACGATTAGAGGTAGGGATCCTGCACACAC
CCTATTTTCCTCCCCAGTGTTCTGACCGAGAGACTAATTAATAATTCAAGGAACTT
ACAGTGAATGANAACCCATGGTTTTGCTTAATTATCAGAACAGCTAGATCTGAGAA
CAGCTGTCTCCCACATGGATAGACACTTATTCCACCCATTTGCAGGTAGAATAGCT
GGCAATAATAAGTCCTTCCCATTGGATATGTTGAAAGGTGCCTGCCATGGCATAGT
TGCCACAAGAGAGGAAGAAATGGACACAAATGTAGGCTGTTTTCAGGGCANAGGGA
AGGTGGGAGGAAACCAANTTGCTGGTTTTCACACACCCTCTGGGGAACACCCATGC
ACCTATGANATG

Sequence ID 527

GACAAAAGCTGAGAGAATTTTTTCTTGAATATTTGCACTAAAAGATAGGTTAAAA
TTCTTCAGGCTGAAGAGAGCATACCAGGTGGAGATTTGGATCTACAAAAAGGAAGG
AAGATTTGGAAATGGATTTGGCACCATTGACTCAATTTCCAGAACAAGAAAGCAGG
GACAGTTTTGGGAAGCTCAAGACACACTGCCCATGAGCAGCAATTTGGACCTCCTG
CTGCATCCACTGTGCATCAAACACACACTGTACAGACAAAGACTCCCAGGAAAAGA
AGTATAAACATGGACTAACACAGAGATGGGCAAACTACAGCCTGTGACCCAGCCAC
CTGTTTATGTAGAATCCAAAGTAAGAATCTTTAACTTACACATAAACTT

Sequence 529; 660nt

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA
ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT
AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGTACCATGAAATA
TCCAGAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAACAA
ATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA

Sequence ID 529

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA
ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT
AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGT

Sequence ID - 530 nt: 660

GACAGCAGAGCACACAAGCTTNTAGGACAAGAGCCAGGAAGAAACCACCGGAAGGA

ACCATCTCACTGTGTGTAAACATGACTTCCAAGCTGGCCGTGGCTCTCTTGGCAGC
CTTCCTGATTTCTGCAGCTCTGTGTGAAGGTGCAGTTTTGCCAAGGAGTGCTAAAG
AACTTAGATGTCAGTGCATAAAGACATACTCCAAACCTTTCCACCCCAAATTTATC
AAAGAACTGAGAGTGATTGAGAGTGGACCACACTGCGCCAACACAGAAATTATTGT
AAAGCTTTCTGATGGAAGANAGCTCTGTCTGGACCCCAAGGAAAACTGGGTGCANA
GGGTTGTGGANAAGTTTTTGAAGAGGGCTGAGAATTCATAAAAAAATTCATTCTCT
GTGGTATCCAAGAATCAGTGAAGATGCCAGTGAAACTTCAAGCAAATCTACTTCAA
CACTTCATGTATTGTGTGGGTCTGTTGTAGGGTTGCCAGATGCAATACAAGATTCC
TGGTTAAATTTGAATTTCAGTAAACAATGAATAGTTTTTCATTGTACCATGAAATA
TCCAGAACATACTTATATGTAAAGTATTATTTATTTGAATCTACAAAAAACAACAA
ATAATTTTTAGATATAAGGATTTTCCTGGATATTGCACGGGAGA

Sequence ID 532
GAATTGTGATAGTTCAGCTTGAATGTCTCTTAGAGGGTGGGCTTTTGTTGATGAGG
GAGGGGAAACTTTTTTTTTTTCTATAGACTTTTTTCANATAACATCTTCTGAGTCA
TAACCAGCCTGGCAGTATGATGGCCTANATGCAGAGAAAACAGCTCCTTGGTGAAT
TGATAAGTAAAGGCAGAAAAGATTATATGTCATACCTCCATTGGGGAATAAGCATA
ACCCTGAGATTCTTACTACTGATGAGAACATTATCTGCATATGCCAAAAAATTTTA
AGCAAATGAAAGCTACCAATTTAAAGTTACGGAATCTACCATTTTAAAGTTAATTG
CTTGTCAAGCTATAACCACAAAAATAATGAATTGATGAGAAATACAATGAAGAGGC
AATGTCCATCTCAAAATACTGCTTTTACAAAAGCAGAATAAAAGCGAAAAGAAATG
AAAATGTTACACTACATTAATCCTGGAATAAAAGAAGCCGAAATAAATGAGAGATG
AGTTGGGATCAAGTGGGATTGANGANGCTGTGCTGTGT

Sequence ID 533
CTTGAACCTCGGAGGCAGAGGTTGCAGTGAGCCGAGATCACGCCACTGCACTCCAG
CCTCGGGGACAGAGCAAGACTCCATCTCAAAACACACACACACACACACACACACA
CACACACACACACAAAACAGATATACACTGAACACAGCACAAGTGGGACATAAGAG
ATTTAAAAGGGTTAGAGATGTAAAATGGATCTAGGAATGGAAACCATAAGGNGGGA
TTTATCAACTGGATTCTGCANAATGCTGTTAAGGCCAGATGTTAGCAGGTGTTACA
TAAAAAAGGGATACCATGAGCAAAAGTATTTGAACATGGGCAATGGTTGAAACAAG
TTTAAACAGATTATNTTTATTACCAAATCTCTCAAACCTTTAATATGCTATAAACA
TTGTGAAACAATAAAAAAACTTTCCAAAA

Sequence ID 534
GGGAAGGGAGCTATGAGTGTGTGTGTTGTGTATGGACTCACTCCCAGGTTCACCTG
GCCACAGGTGCACCCTTCCCACACCCTTTACATTCCCCAGAGCCAAGGGAGTTTAA

GTTTGCAGTTACAGGCCAGTTCTCCAGCTCTCCATCTTANAGAGACAGGTCACCTT
GCAGGCCTGCTTGCAGGAAATGAATCCAGCAGCCAACTCGAATCCCCCTAGGGCTC
AGGCACTGAGGGCCTGGGGACAGTGGAGCATATGGGTGGGAGACAGATGGAGGGTA
CCCTATTTACAACTGAGTCAGCCAAGCCACTGATGGGAATATACAGATTTAGGTGC
TAAACCGTTTATTTTCCACGGATGAGTCACAATCTGAAGAATCAAACTTCCATCCT
GAAAATCTATATGTTTCAAAACCACTTGCCATCCTGTTAGATTGCCAGTTCCTGGG
ACCAGGCCTCANACTGTGAAAGTA

Sequence ID 560

GGCGGAGGTTGCAGTGAGCTGAGATGGCGCCATTGCTCTCCCAGCCTGGGTGACAA
GAGCAAAACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAGCAATTTACTTAAAAAC
ATACAAACACAGAGACAAGTATTTTTGAGAAACAAATACCTTTTTCATTTTTTATA
CCAATGTAACAATAATCCATTAAACACACCTTTACTAACTGTTTTCTAGGAGTCTG
ATATGATGAGGAAATAGGTAAACCTTTAATAGCCAGTACTAAATTAGAGTGGCACA
ACTTTCACTGGGAAAAAAGATGGGTATTTTACTTTTCTGTTTTAGAAAAGTGGCTT
GACAACAGTATGCTTATGTCTTAGAGTTTGAAATTCAAGTTCTTGAACATTATTAA
TGGCTACAATCATTCATACCCACATTGGGCTGTATTCTTGATGAATCCAAAGTGAT
TTTCACCTCAACTCTGAATTTCATTCTCCTCTTTTGAATATAATACAACCATCTCA
CTAGAGGAAGCATTTCAGTCTTTTCTGATTGGAGATTCATTATTGTTTTAGATAAT
GTTTTCATTTGCTTATGGGTATATAAAAAATTTTATCTTAAAAATATTTCCTCTCA
TTTAGCTAGCAACATTGTTTTC

Sequence ID 561

CTCAGGGTGATCTCTGAACCCAAACTTGCCCCAAAGAAGGTTGCTCTGTCCTCTCC
ACATCCCCATCTCCTCCCTAGGGCCTTGTTGGGGAGAGGCTCCTCCATCTTTCCCA
AGTCACACCATCGTTTCCTACGTGGTCTGGACAAGAGCAAGAGCACACCTTGTCCC
CACCTTCTCCAGAGCAGCCAGAACCCACCTCAGGTGCCTTCCCCATCCGGTGCAGT
TAAGGCACTTCTGCCAGCACCATGGTATGAGCACTAGACTTGGAGTTAAGATTTGA
GAGCCCCCTCTGTCACTGTGGAAGCTTGAGCATGTTGCTTGATCTCTCTGAACCTT
GTGTTTCTCATCTGTGAAAGGTGATAATGTGGGGCTGCTGTGAGATTTAAAGGACA
TAATGCACCTACGGTCCAAGCACTGCCTGGAATACAGCANAAGCTCAACAGATACT
GGACAACCCATCCCCTTAGTAGAGGCACTAACCATGTGACCCAAGGCAAAAGTGCT
TAAAAAAA

Sequence ID - 562 nt: 580

ATTGCATGCAAGTTTGCTGAGCTGAAGGAAAAGATTGATCGCCGTTCTGGTAAAAA
GCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGATGCTGCCATTGTTGATATGG

TTCCTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGC
TTTGCTGTTCGTGATATGAGACAGACAGTTGCGGTGGGTGTCATCAAAGCACTGGA
CAAGAAGGCTGCTGGAGCTGGCAAGGTCACCAAGTCTGCCCAGAAAGCTCAGAAGG
CTAAATGAATATTATCCCTAATACCTGCCACCCCACTCTTAATCAGTGGTGGAAGA
ACGGTCTCAGAACTGTTTGTTTCAATTGGCCATTTAAGTTTAGTAGTAAAAGACTG
GTTAATGATAACAATGCATCGTAAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGG
ACCACTTTGGTTTTCTTTTTTGCGTGTGGCAGTTTTAAGTTATTAGTTTTTAAAAT
CAGTACTTTTTAATGGAAACAACTTGACCAAAAATTTGTCACAGAATTTTGAGACC
CATTAAAAAAGTTAAATGAG

Sequence ID 563
GCAACCTGCACAACCCCGCCCTGTTCGAGGGCCGGAGCCCTGCCGTGTGGGAGCTG
GCCGAGGAGTATCTGGACATCGTGCGGGAGCACCCCTGCCCCCTGTCCTACGTCCG
GGCCCACCTCTTCAAGCTGTGGCACCACACGCTGCAGGTGCACCAGGAGCTGCGAG
AGGAGCTGGCCAAGGTGAANACCCTGGAGGGCATCGCTGCTGTGAGCCAGGAGCTG
AAGCTGCGGTGTCAGGAGGAGATATCCAGGCAGGAGGGAGCGAAGCCCACCGGCGA
CTTGCCCTTCCACTGGATCTGCCAGCCCTACATCCGGCCGGGGCCCAGGGAGGGGA
GCAAGGAGAAGGCAGGTGCGCGCAGCAAGCGGGCCCTGGAGGAAGAGGAGGGTGGC
ACGGAGGTCCTGTCCAAGAACAAGCAAAAGAAGCAGCTGAGGAACCCCCACAAGAC
CTTCGACCCCTCTCTGAACCAAAATATGCAAAGTGTGACCAGTGTGGAAACCCAAA
GGGCAACAGATGTGTGTTCAGCCTGTGCCGCGGNTTG

Sequence ID - 564 nt: 671
GGAATAGAATTTTAAATAGTAATAACTGCTTGTTTTTTTGTGCAAGTACTTTTAT
ACATAAGATAAACAAAAACCTTACCACCAAACATACCAAAATGCACCTCTTTCATA
AGTGAGTTACTAAGATTTCTATACCTGGAATATCATGTATGTTTCATTTACTGGAT
GTTTACATTTTAGGAAGGAAAATAGTTTTGTTTATTTAAACAACTGAATACTTATA
AACTGTTGTTCCTGGAAGTTATTTATTCCATAAAAAATTTGTTCTTTTGTCATGAA
TTTATAATTCCTAAATGAAGACCAGAAAGTACAAATTGCTGGGAGGAAGAATAGGC
TTTATTAATCAACTGATGTCTTGATTTTTCTAAATGGGAAGATTGCTTTATTTTTA
ACACTAATTATGGGAGCAGATTCTTAGCAAACTTCTTTGGAAAAGTTAATGTTATG
ATGTGCATTAGGCTGCCCCATCGTGTATATAAATGAAGCAGATTTGATTTTTGTAT
TCTTACGTTTCTCTGCTTTGTAGTTGTGGCTGTACTTAAAGAAATACAGAATTTCA
TATATTTAAAAATGTTTAAAATGTGACCCACAGACATTGTAAATGGATTNAAAACT
AACATGAAAAATATTCAACCTAAAAGAATTCTTAACTTCACAAGTGTTTTACTTC

Sequence ID 565

CTTGGTTCCGCGTTCCCTGCACAAAATGCCCGGCGAAGCCACAGAAACCGTCCCTG
CTACAGAGCAGGAGTTGCCGCAGCCCCAGGCTGAGACAGGGTCTGGAACAGAATCT
GACAGTGATGAATCAGTACCAGAGCTTGAAGAACAGGATTCCACCCAGGCAACCAC
ACAACAAGCCCAGCTGGCGGCAGCAGCTGAAATCGATGAAGAACCAGTCAGTAAAG
CAAAACAGAGTCGGAGTGAAAAGAAGGCACGGAAGGCTATGTCCAAACTGGGTCTT
CGGCAGGTTACAGGAGTTACTAGAGTCACTATCCGGAAATCTAAGAATATCCTCTT
TGTCATCACAAAACCAGATGTCTACAAGAGCCCTGCTTCAGATACTTACATAGTTT
TTGGGGAAGCCAAGATCGAAGATTTATCCCAGCAAGCACAACTAGCAGCTGCTGAG
AAATTCAAAGTTCAAGGTGAAGCTGTCTCAAACATTCAAGAAAACACACAGACTCC
AACTGTACAAGAGGAGAGTGAAGAGGAAGAGGTCGATGAAACAGGTGTAGAAGTTA
AGGACATAGAATTTGGTCATTGTCACAAAGCAAATGTGTCGAGAGCA

Sequence ID 566

GTCACCAAGAGCTTGTTGTCAGGTTTTCACTTGCTATTCGCAGAGATTTTTTTAA
AGGCACTATTTGTAGTGTTAAAAGGGTGAATTTATCANAAGGCATAATAATCATAA
ATGTGTATATGCCTAATAATAGAACTTTAAAAGGCATGAAGCAACACTCAAAAGGA
TTAAAGGGAGATCATCTCACCCCCTTCTTACCAATTGATAGAATGATCTGATGAAA
ACAGTAAAATAACAACAGATCTGAACACTGTCAACCATCTTGACAAATACTTATGC
CTAGTGTTCCATTATTGGAACACTAAACATGTGGAATGATTTATATCCTACTGCTC
AAGGTCATCACCAAGGTCTAATTGTAAAATTTCAAAAAATTGCAACCTCAGGCATA
AATGGGTTAATCGACATTTATAGCACACACATGCAACATGTACCAGAGATTCCTTC
TTTTCTATGAACATGGTACTTCCACCAAGATAGACCACATTGTGAACTATAAAACA
AATCTAAAAACATTTGAAATGAAGGAAATTATATAAAATATGTTCTCTTGATCTCA
ATGAAATTAAATTAATACTATAT

Sequence ID 567

CTCATGGCGGCCAATGTAGGCCCAAAACTTCCTCAAGTCAAACTCTCCAGGCCCAC
CTTCTGCTTCCCGGTGGCATCAACAGGCCCAGCTTTGACTTGAGAACAGCCTCTGC
AGGCCCTGCTCTTGCCTCCCAGGGGCTTTTTCCAGGCCCAGCTCTTGCCTCATGGC
AGCTGCCCCAGGCCAAATTTCTGCCTGCCTGCCAGCAGCCTCAACAGGCACAGCTC
CTCCCTCACAGTGGCCCATTTAGGCCCAACTCATGACTGTGAGGCCATTTCCAGGC
CTAGTGCCTGCCTCGTGGCTGACTCTTGAAGCCCAAAACTTCCTCAAATCAGCCTT
TTGCCCAACTTCTGTCTACTGTCGGACTCTACAGGTCAGCCTCTGCCTCACAGTGG
ACCCTCCAGACCCAGATGGTGTCTNCTGTGGCATCCTCAGGCGAAGCTCCTGCCTT
TCGGCAGCCTCTCCAGGCCCAGCTCCTCCTGCTCCAGCCTTCTCTCCAGGCTCTGA
ACTTTCTCAGGTCTCCCTCTGTTGTCCAAGGCTGGAGTGTAGTAG

Sequence ID 568

TATATATGTAATGCCCTTAACCTAGTGTTTGGCATGATCGTTGCTGAAAGGGAAGC
TTGTGGGTACAGTGTCCCCTCAGAAGCCAAAGCCCAGGGAAGGTCGCCTGCCCAGG
TCAGGCTCCCAGCGAGTTTGTCTGGGGAGGGGCCATTCATACCTCCAGGTCAGGAC
AGAGGCTCGGGCTGAGGGAACCCTACACAGGTCCTGGAAGCAGATCCTTCCTGCCT
AAGCCAGCAGGACAGCTCAACAGGAAGCATCTTCCAGCCACGGGAGGAGAGGCAGC
ACCTTTTTTGGAACCATACAGAGCTAAGAATGGTGGTACAAGTAATAGATTCTGTA
CTGGCAACCCCACTTGGTGGAGCAAGTTCTAGGAAAAGGGGGCTGTCCTTGAGTCA
GCCATGGGGTCAGCCACACAGTCACCGCAGCTGCTCTTTGGCACCGGGCGCTGGAA
AGACCTAGGATGACACAGCCTGGAAAGAGCTTGGGAAAAGCTCATCTTCCACAGAA
CTACCTGCTATACCAGCCAGGGCAGGTGCTTATTCCCACAACAGCCCTCTGTTGTA
GGCGGCAGTGCCATCCTGAANGTGCCGTGGTACCTTCTGAANACCCAGCTGAGGGC
CTGTAATGGCACTTGCATGCCACATGGNACACCCTTTCCCGGTTAA

Sequence ID 570

ACCGCGGCCGCGTNAANAAAAAAAAAAAAAGAATTCCACTTGATCAACTTAATTCC
TTNTCTTTATCTTCCCTCCCTCACTTCCCTTTTCTCCCACCCTCTTTTCCAAGCTG
TTTCGCTTTGCAATATATTACTGGTAATGAGTTGCAGGATAATGCAGTCATAACTT
GTTTTCTCCTAAGTATTTGAGTTCAAAACTCCTGTATCTAAAGAAATACGGTTGGG
GTCATTAATAAAGAAAATCTTTCTATCTTAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

Sequence ID - 571 nt: 457

TTAGAGAGGTGAGGATCTGGTATTTCCTGGACTAAATTCCCCTTGGGGAAGACGAA
GGGATGCTGCAGTTCCAAAAGAGAAGGACTCTTCCAGAGTCATCTACCTGAGTCCC
AAAGCTCCCTGTCCTGAAAGCCACAGACAATATGGTCCCAAATGACTGACTGCACC
TTCTGTGCCTCAGCCGTTCTTGACATCAAGAATCTTCTGTTCCACATCCACACAGC
CAATACAATTAGTCAAACCACTGTTATTAACAGATGTAGCAACATGAGAAACGCTT
ATGTTACAGGTTACATGAGAGCAATCATGTAAGTCTATATGACTTCAGAAATGTTA
AAATAGACTAACCTCTAACAACAAATTAAAAGTGATTGTTTCAAGGTGATGCAATT
ATTGATGACCTATTTTATTTTTCTATAATGATCATATATTACCTTTGTAATAAAAC
ATTTTTCCC

Sequence ID 572

CGTCTATTTGNGTTTCTTCTCACAATTGGTAAGTTCTCTGTATTGATTGATGGCTA

AGTTTGATTAGTGTTTTTCTCTAGTTGGTAATTATATTCTAGTATTTTATCATCTT
ATTGTTTACTCAACTNAAAGTGNCACAGAAGAGTTGCCAGGTTTCTCTTTGATATG
AGATCTCTNNTTGATTTGGAATGCAAATCANAAGTGTCATGTTTTGAATAAAGGGA
CCAGATGACTTATAGGTATTCTTTCTCTAAATATAACTAAGGTAAGATTTTTGTTT
TGAGGTACTTAATCTATATAAGTGGTAAAGAATTTACTTGAATTTCTCCAAATTCT
CATGTCTAAAGTCTGATTGATTAAATTCATTCTTGGTATTTCATTTTGAAAAGAAT
GTAGCTTTAGCAAACCTCTTTGTATAAATGCAGTGGGATTAAGGTCATTTAAAAAA
TTGTTATATCATTGTATTTTTAAAATTTACCAGTTTTATTTTTCTTTTTACCCTTT
AGCCCGGCCTCAGAAAGTGTGTTTGTGTCCATTTCTCCCAGCGCACCCTCTGCATA
TCTCTACCCACTTGTCATAATTCAGCATCCAGCAGAGGAAAACAAAGTGTTGCGTA
CAGTTCCTCTACTAGCAGCATGCCTCCCCCAGGACAAGTGTA

Sequence ID 574
TTATTGCTGACATAAAAATGGTGCACATCGGCCAGGGCCCAGGATGAATCAGCCAA
TCTGCACCATTTATACATGGAACTGGAGAACATTGTGCCAATAATCATTTAATATA
TGCCAAATCTTACACGTCTACTCTAAACTGCTCTAATGAAGTTTCAGTGACCTTGA
GGGCTAAAGATTGTTCTTCTGGGTAAGAGCTCTTGGGCTGGTTTTTCANAGCAGAG
TTCTTGTTGTGGGTAGACTGTGACTAGGTTCACAGCCTTTGTGGAACATTCCGTAT
AACGGCATTGTGGAAGCAATAACTAGTTCCTATGAAAGAACCAGAGCTGGGAAGAT
GGCTGGGAAGCCAGGCCAAAGTGGGGGCAACAGCTTGCTTCTCTTTCTCTTCTCAC
CCTCAGTTTGTATGGGAAAATGGAGATGTCCTCTCCACTTTATCCCACGATATCTA
AATG

Sequence ID - 575 nt: 209
CAGGATATCGAGACCATCCCAGACAGCATGGTGAAACTCCGTCTCTACTGGAATAC
AAAAAGTTAGCCGTGTGTGGTGGCACGCGCCTCTAATCCCAGCTATTCGGGAGGCT
TAGGCAGGAGAATTACTTGAACCCGGGAGGCGAAGGTTGCAGTGAGCTGAGATCGC
ACCATTGCACTCCACCCTGG-CGACAGAGCAAGACTCCGTCT

Sequence ID - 576 nt: 541
CAGCCAACCCAGAAGGAGCCAGTCTACAACTATGCCTGATCCTCCTCATGGCAGGC
CACGAAGCATTGCTGCCATGTGTTGAATTATAAAACCCACATTGCTTTTTGAACCC
TGTTGCGGGTAAAAATAACCAAATTATCAGTCCTTGGAAACCCAGGCAATCAAGTG
AGTACAAGGTAAAGATAAGTATGGTTTAGAGGAGAAATTATGTTCCTGAACTGGTG
TCCTTTGATGGCAGCGTCAGCCTTGCTAAGTCAGAGTAGAGGGAGCAGTGACCTTA
ATAAGCTTTGGTGAGCATCATGTGCACGCGTGGGTGGGAGTCCCTTTCACTGATGC
TTTTAAAAGTGCTTTTGCAGACCCTGGAAGGGATCCTCCACACATATGAGGTGTGG

GACAGGTAGGCCAGAGAGGATTAGCCCTGCTTTCGAGACTAGAAATCTACAGTCCT
GAAGGAGCAGTAATTAATTGGTACACCTGTCAGGGCCAGCCCCCAGGTCTCCTGGC
TTTTTCCAGGTTTTCTGTCTCACATGATTTTGCTTTT

Sequence ID 577

CTTTAATTTTTCAAGTGTTTAAAAAACAATTTTATACTTAAGCCAGCCTTGAAGAT
AAGCACAAAATTTACCAGTTTACATTTAAAAAACAAACAAAAAACGACAACAACTC
AAGCACCCGCTCTGTGCATAGCACTATTCTAGGTGCAATAAAAGGGAATCTTAACC
TTAGAAATATGAGTTCACTTTCTGGAATTGTATTATCTCCTTTTCCAGAGAGTAAA
AATAAATAAAATCACCATTGTTTACTACAGATCTGCCCCAAACCACATCTGGTTCA
CAGAAAGGCTAATTTCTGCCAAATTAAAGATGTAATGAACTCAGTTCCTGCTTTCC
CAAAAACACGAAAGCAGAATTCCTTTTCACTGAAAAAAATAAACAGTTTTCCATGC
AAGGGCAGTTTGCTTCTAATAAGTATTTTTTAAAAAATTTTTTTTCCTCTAGCTT
TTCTTTAAATTTTCTTCCTCTAATATTGCCTTTTCTTGTACAAGGCAGACCAGGTA
TCTTTTTATGCTGTTTTTCCTTTACTAAGAAAAGTATTGCATCTTGAAGACAAACC
ATTTCCCAGAGTAGTGATAAAAAATAACACTAAAAAAACTTTAAAGGTGAGTCACT
TCATCACCTTGATGAAGTAAAAAA

Sequence ID 578

GGAAAAAAATATTTCCACTTAGATATTTTACATGGTTTTGTTTAAAATTACCATTAC
TTGTTTTTTAAAAACACATGACCACATATGTATATGTATATCTACCTAAACATTGT
ATCATGGTTTCAGTATGTTATTCATGTATTACTGGGAGATGCTACCAAGAAACCAA
CCCAAAGAAAATTCTGGAAAATACATTTCTATTTATAGAATAAATGTTTCATTTAT
ATAAAAGCAAAAGAACTTAGAGTTCTAATAAATGGGATGTCTAATAAATTATGAAG
TTACTGATTTGAATATATTATATTTTTATAACTTCCTTGCCAAAGTCCTGATTTAG
TACATTAGAGAACCTGTGTTTCCTCTCTCCTCTACCATTCATCTCTCTTCCATACA
GTCATTTGGGCTTTTTACTCAAAGAGAATCAAGAAATAATAAGGTATAACAAGCTT
GGCAAAGTGTTGGCTTTTTAAAAAAAAATTTTTTTAATCTCTAGCAGTTTGGTAAT
TTAGCAGCATCATTTATTTGGGATTCTTTTATCTGATTTCAACAGTGAAAAACATC
CCTATGATAAAGCCTAATGACCCATTTCCAAAAGATGGAATTGCCCTTCCTAGAAA
ATATGACGGAGAAAAGT

Sequence ID - 579 nt: 502

CGAATAGCCAAGTGGTCTGACAAGATCGAGAGTAATGAGGCCCATACTTTAGTACA
GTCTTGAATGGCCAGATGGTGCTGGGCATACCCCAACCAGAGATATGTAAGTCTTT
ATGTTGTCAAAATTTCCCAGAAACATGAATTTCCCACTAAGATTCATTAAGGAAAA
CTAGAATGAAAACAAAAACGTTCCTTGTATAATATTCATTANAAAGAAATGAAGAA

GGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGAGAGGCCAAGGTAGG
CAGATCATGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAATCCCGTC
TCTACCAAAAATACAAAAAAATTAGCCGGGCATGGTGGCACACACCTGTCATCCCA
GCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGTGGAGGTTGCA
GTGAGCTGAGATTGCACCACTGTACTACAGCCTAGGTGACAGTGCAAGACTCTG

Sequence ID - 580 nt: 316

CCTATGCCAAACTAAAGAAAGCTTGCCTGGCCTACAGGCCTAAAGGTTCAAATGNG
GATTAAAAAAACACAGTAGTCACATAAAATGTCTGCTGGCTGGCTGGAATTCCATC
ACCTACAATTTACCTGCTTTCAAAAACTGTGTTCAACATTGAGAAAACAGAAAACC
ACTTATCTTGAGCTTAATATGGGCTTCTTTTTCCTTAACTGTAGAACACTTACTGA
AATATCAAATCAATGGTTAGGATATGTATCCTAGGCAGGCCTAAACCATTAACACT
TGGTTTAAGCAACTTTGTATAATTNACCTCCTAAAT

Sequence ID 581

CTTCATGAGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCA
CACATCCAGTCAGTCACTCATCAACTCTATTGATTCTG-CTGCTAAATATATCTCA
ATTGTATTAACTTAAACATATGCATAATACATCTTCTTCTTCACTGCATTTTTGTG
GGCTGCACTTACCTTTCAGGTAACAACAACACTGGCCCCTCTTGCCCTTCTAGTCA
GAAGTGCCAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAACATTACACTG
AATGTGCAAAACTGGAAGGGCATCCAAACAGAGGAGG

Sequence ID 582

TAGAATTCTCGCCTGCCTTGGCTTCTCCCTCTAGTTGTTCCTTCTCTGTCTTCTGT
GGGCTTCTTATTGTCTGCTCACTCCTTCTTCAGTGTCCTCTCATGGGCTTCCTTCC
CTTCTCAGCTGATGCCATCACCTGGGGAATCACAGTTACTCAGCAGCACTGGGGCC
TCTCTATCTCTATGCTGGTCATGCCTATGTGTGAGCTGCAGACCCAGTGGAATTTC
CATTTGTGCATCCCATGCCCAGCCCACCCTCCACCAGCCTCGAATGCAGCTGTTCA
GCCCTACCCCAGTCCTCAGAAAAGTTCCTCTCCCTGGATCCTCTTTTTCCTTCATG
AGTGCCCGGTTGCCCAAGTCAAAAACCTGGGAGTGATATAAACTCCCCACACATCC
AGTCAGTCACTCATCAACTCTATTGATTCTGTCTGCTAAATATATCTCAATTGTAT
TAACTTAAACATATGCATAATACATCTTCTTCTTCACTGCATTTTTGTGGGCTGCA
CTTACCTTTCAGGTAACAACAACACTGGCCCCTCTTGCCCTTCTAGTCAGAAGTGC
CAAAATGATGAGAGCTAGCCATGACAAACCCACAGCCAACATTACACTGAATGTGC
AAAACTGGAAGGGCATCCAAACAGAGGA

Sequence ID - 583 nt: 631

CTGAGGTGGGAGGATTCCACTCTCACCCATTTCTTCTTTCATTTTCAGTTTCTCCA
GTTAGTAACTGAAGATGTTCTTTGAGTAATTAAGTGAGTGAGAAAATTTTTAAGTG
AGAAATCTATAAAAAGAACCATGTTAACATAAATATTTCAGTCCTTACAAGTTGGT
ATTGACTTTTCTCATTGGTAATCTGACTGATTTAATACTGCTCATTCCAATATCTG
GTGATGTAATTCTGGTTATGAATCCTTGTATTAATAACACCTCCTGGGAGGTTTTT
TTTCCCCAACATTACATTCAGAATATTAGAGCTGAAAATACCTTTTTAAGGTTAT
CAGGAGGAGGGAGCTTATGTTTAATGTGGTGGATAAAACTTAACTGCTGGTTAATA
CAATTGTTATTCAGGTGAAATTCCCTAAACTTTTCACGTGCAAAGTTTTGTATGTA
TACAGACATTTGGGGAAAAGTTTTATCATCCCTAAAACCGGTTACTGTCCAGAAAA
TGATAAGAATCCCTGGGTTCCAAATCCTTCATAAGGTATTTATTCATTTATTTATT
CAACACATTTACTCAATGCCTCCGCTCTGCTGCAACTACACTGACATTCTGCTTCT
AATCTAACCGAAAAT

Sequence ID 585

TTTCAAATTGTACAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGA
TTAATGGACAAAAGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGC
TCATAAAAATCATGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATA
TCTTACACAATCTTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATC
ATGGTAATTTTATGCAAATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTC
TCAGTTCTGTTATTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATTGGCA
AAGGGCCCTAAAAAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTC
CTAATTTGAGATCACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTC
CATAAACCAACAAATAATTTGGCTGTAATGTATCATAAAACACAAACCCCACACAT
CTGTACAATAAACATTATGTATTACATACACACAACACACACCCAGTCATAAAGCC
TAATGATGTGCTGCTTCCAGTTCAATATTCAGCTGTGCATTTTTTCTTATTTCATC
AAATGAATAGCTTTTTGTCACC

Sequence ID 586

GTAAACTGTTCTCTCCGAGGGAAAAAATGGAAGTTATCCTCACAGTTCACTGCCGT
GGTATTTCTTCTGTCCCATGCTTTGCATGACTGCCATGGTACAGCCTTGTTTCAAA
CTGTTCACTGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAA
GAAGTAGTTCCAAACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAG
AGAGCAGCTTTAAAAGGTACTAAGCCTTTTACAAATTGGTGAGTACTGGCACATGA
GAT

Sequence ID 587

TTTTTTTTTTTCCTTAAAAGGTAACCCCTAAACACAGCTAAAACTATGCCATCAGC

TGACTCCAAGGNACACACAGTCCTGTATCTGGAACTACTGAGTGGCAGGCATCTTT
CTCTGCCTCTGACAGTGGAGTCCCCATCACTGCAGAGCATAGCCAAAGGAGTCAAA
GGTCTCAGCGGGTCACTGCCTTATCAACCCTCACCAGTCCCTTATGTTTTTAATA
TTTTATAATCTTGACATGACACCAAGATGCTTTAATAAAAAGCACCTCTAACTCG
GTCTTGTATTCACTTACCTTGAGCCTGGGACTTCTCTAGGCTCCTGAGGCAAAAAC
AGGTAGAGGGGAGATGGTGGAACATAAAACACAATTTTGCTTGGCACCCACCTTGG
CGTCTGTCCCCATGACCAGGTCTTTCAATTCGATGATTTTGTCATTGATGGAGGAG
CGATATCGTTTCTCAATGATATTATGGGTTGTCCGCCTTTCTCCTTCTTTGGGGGG
CTCAAGCTGCTTGACTCCCCCAGGTACCTGCTTAATGGGGCACTTTCTCTTGCCCC
ATCATTACAGGCATTGTGGTCAGAATGGTCCCACTGCTGCCCACCAGGGTCTA

Sequence ID 588

CTAGTCTTTTCATAGTCTGCATAGAGTCTGGCCATTACCATCAGTTTTTAAGATGT
CCATATTGTGGCCGGGCGCGGTGGCTCACGCCTGGTAGTCCCAGCACTTTGGGAGG
CTGAGGCAGGTGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTG
AAACCCGTCTCTACTAAAAAAAATATTAAAAAATTGGCCAGGCCTGGTGGTGGGCG
CCTGTGGTCCCGGCTGCTTGGGAGGCTGAGGCAGGANAATGGTGTGAACCCGGAAG
TCGGAGGTTGCAGTGAGCCAAGATTGCACCTGGGCAACACAGCGAGACTCCGTCTC
AAAAAAAAAAAAAA

Sequence ID 589

CAATTATTTATTACCTTTCCATTTGTTCGCCTGATGATGTGACAATGCATGGTCTT
TGTGCATGCTGCTAGACACTTTTCTTTCCCAGCCGAAAAGTCTATTATGTAATTTT
TACATTCATAATTTTAATGTGGATGATCAGGATTAAATCAAGATATATATCTGGAA
CCTCTTATAAATGGAGCACTTAGAAATTTGTTGTTCTGCACTTAACCTAGAGAGAG
AAAAAATGCTTTTCTTTGTGAAAAATCTGAATTCCTGTCCTGACCTTCTGTGATGT
GGAAACCCTAGGCTCTGAGACACACTCTCTGGTGTCTGAGACAGAACCAAAGCAAT
AACGTTGTGATGCCCACAGGCCTGGAGCCAGCTAGCGACCTTGTGCCGCCCAGCTG
TCCATGGCCCGTGCAGAGCAGAGGACAGTGAGTGTCTGCACTGAGAACCTTAAACC
ACAGTTGAACATACCCACACCTGTTTGTCTTAAGCTATAGTGTAAAAACAAAGTTT
GGGCTCTGAAAATTTAACTGAAAAAGATTTCCTTGTT

Sequence ID 590

GTGGCAGCAGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGG
ACCTGTACGTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGAC
CACGCATCCATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAA
TGGCCAGTTTAAAACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAG

ATGATTCCATTCTCCGATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGA
CTGGAGAGAATCACAGATGTGGAATATTTGTCATAAATAAATAATGAAAACCTAAA

Sequence ID 591
CAGCAGCAGAAATGTTTGCAAGATAGGCCAAAATGAGTACAAAAGGTCTGTCTTCC
ATCAGACCCAGTGATGCTGCGACTCACACGCTTCAATTCAAGACCTGACCGCTAGT
AGGGAGGTTTATTCANATCGCTGGCAGCCTCGGCTGAGCAGATGCACAGAGGGGAT
CACTGTGCAGTGGGACCACCCTCACTGGCCTTCTGCAGCAGGGTTCTGGGATGTTT
TCAGTGGTCAAAATACTCTGTTTAGAGCAAGGGCTCAGAAAACAGAAATACTGTCA
TGGAGGTGCTGAACACAGGGAAGGTCTGGTACATATTGGAAATTATGAGCAGAACA
AATACTCAACTAAATGCACAAAGTATAAAGTGTAGCCATGT

Sequence ID 592
TACTCAATGAAAAACCATGATAATTCTTTGTATATAAAATAAACATTTGAAAAAAA
AAAAAAA

Sequence ID - 593 nt: 565
CAGGATCAAGGTGAAAAGGAGAACCCCATGCGGGAACTTCGCATCCGCAAACTCTG
TCTCAACATCTGTGTTGGGGAGAGTGGAGACAGACTGACGCGAGCAGCCAAGGTGT
TGGAGCAGCTCACAGGGCAGACCCCTGTGTTTTCCAAAGCTAGATACACTGTCAGA
TCCTTTGGCATCCGGAGAAATGAAAAGATTGCTGTCCACTGCACAGTTCGAGGGGC
CAAGGCAGAAGAAATCTTGGAGAAGGGTCTAAAGGTGCGGGAGTATGAGTTAAGAA
AAAACAACTTCTCAGATACTGGAAACTTTGGTTTTGGGATCCAGGAACACATCGAT
CTGGGTATCAAATATGACCCAAGCATTGGTATCTACGGCCTGGACTTCTATGTGGT
GCTGGGTAGGCCAGGTTTCAGCATCGCAGACAAGAAGCGCAGGACAGGCTGCATTG
GGGCCAAACACAGAATCAGCAAAGAGGAGGCCATGCGCTGGTTCCAGCAGAAGTAT
GATGGGATCATCCTTCCTGGCAAATAAATTCCCGTTTCTATCCAAAAGAGCAATAA
AAAGT

Sequence ID 594
CAGAAGAGTAAGCAAATCTCAAAGCAGCGAAAGGGAAGAAACTAAAAAAGGTAGAG
CAGAAATAAGAGAAAATAGAGAAGAGAACAATTGAGAAAAATAATTGAAACCAAAA
GGTGGTTCTTTGAAAAGCCTAACAAAATGGACACATCTTTAGTTAGAGTGACCAAG
AAAAAAGGGCAGTGACTCAGATTACTTCATTCAAGAGTGAAAGAGGGCACATCACT
ACCAATTTACAGAAATAAAAAGGATTATGAGGAAATACTACAGATAATTGATGACA
TTAACTTAGAAGAATATATTTCAAGAAAGACACAAACTACTGAAACCGACTCAAGA
AGAAACAGAAAATCTGAACAGACCTATAAAAAATAGAGATTTAATTGATATTCAGA

AAGTTTCCCAAAAAGAAAAGCACTGGCCAAGATGACTTCACTGGTGAATTCTATCA
AGTGTCAAAGATGAATTACTGACATTCATTCACACTCCTTTAAGAAATAGAAGAGG
GGACATCACTTTTCAAAGCATCGACATTCTAATCATTAGTCCCTTGGTTTCCTGCT
CCCAAAGCCAGGTGATGTATCACAAAAAAACCCCTACAGACCCACTGGGCACAATG
GCTTTATGCCTAT

Sequence ID - 595 nt: 98
CTTTGCTCGAATNGTCAGATAAGGATTCTGTGAANGGAGATGAGATTTCCATCCAT
GCTGACTTTGANAATACATGTTCCCGAATTGGGGNCCCCAAA

Sequence ID 596
CTCAAGTGTTCCCTCAGCTTAGGCTTTGTTTAAATGATCCCACCCAGGGGCGATGG
TAGGGAACAACAGGGTCACTAAACTATTTGGCTGGCTACAACTCTGGGAAATGGTA
AGACAGGGAAAGGCCATGTTGTTCATTCCCTTGTGCAGATCTAGGGAGAACCGCAG
AGAGAACAGTTAGCATTTCTTGTTCAATGAATTATCCTATTAAGAACACTGGATGT

Sequence ID 597
CGGNCGCGGTCGACGCTACTCCTACCTATCTCCCCTTTTATACTAATAATCTTATA
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Sequence ID - 598 nt: 362
GGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCAAGAGT
TCAAGGCTGCAACAAGCTTTGATTGCGCCACTGCACTCCANCCTTGGCGACAGACT
AAAACGCTGTCTCAAAAAAAAAACAAAAACGACNAAAAAAAAACAAAACAGAAAAA
ATTAACTTAGGCAATGACAGTCCCTGGCAAATGCTGGGAGGGAGGCAACANTGGTC
AAGGAAGGTAACCCTGAANCAGGACTTGTAAAGCAAATAANATTGGGAGGCCAAGG
TGGGTGGATCACNAGGTCAGGAGTTCGAGACCAACCTGGCCAACATAGTGAAACCC
CGTCTTTCTAAAAATACAAAAAAATT

Sequence ID 599
GACAAAAGAACCATTTGGATACATAGGTATGGTCTGAGCTATGATATCAATTGGCT
TCCTAGGGTTTATCGTGTGAGCACACCATATATTTACAGTAGGAATAGACGTAGAC
ACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGTCAA
AGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTGCAG
TGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGCATT
GTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGTAGC
TCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCTTCA

TTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAAATC
CATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTTTCT
CGGCCTGTCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCACAT
GAAACATCCTATCATCTGGAG

Sequence ID - 600 nt: 595
TTCAAATTCTTGNTAANAGTCTTTGTTCTGAATTTTACTTTGTCTGTTATTCCTAT
AGCCTTTCCAATTTTCTTTCGCTTGGATTTTACGTGATAAGTTTTTTCCCCCATTT
TACTTTTANCAACTCTATATTTTTTAGTTGAGGTTGGGTTTCTTGTAAACAGCATA
TAATTTGGGTTTTTTAATCCAATCTGAAAATTAATGTCCTTAATTTTGTGTTTATA
CCATTTACACATAATGTACTCATATATAAGGTTTAACTGAAACCTACTATCTTGCT
AGTTGTGCTCTACTTGAATTTTTTTTTAGTATTCTGTTTTAATTGACCAACATTTG
ACTGTATCTCTTTGTGTAATTCTTTTACAGGTTGCTGTAGGCATGACAATATATAC
ACTTAACTTTTCTCAGTACACTGAGAGTTGAAATTGTAGTACTTCGAGGAAAACAT
AGAAAACTTGCAATGATATCGGTTACATTTTACCACCTCCATATGTTGCAATTATT
AAATGTATTAGATCTGCCTACCTCGAAAACCCATCAGTCTTTTAACTTTGCTCTCA
ATGGTGATTCATATTTTTAAAAAAACTTGAGGCAA

Sequence ID - 601 nt: 522
TCGACCGGGTTTGGAGCAGTGCCTTGTTTGCTGTGCAGCGGATACTCTACAGGTAC
ATTTCCTTTTTGGAACCAAAAGGGAGGGATTTGACAATATTGATGGTAGATCTTTT
TTCTTTAGCAAGAATTAAGGATTTTGGTGGGTGGGGGGAGGCTTCTGTGGGGACCA
AGACAATGTACTGTCAGTCAGGATTTAAGTCGAACTACCTCATCCCTTGCCCCAGA
GAACAGTTGATCGTGTTTTAAACCAAAAGGTGCGGAATGGAGAGAGGGAGGCGGTG
CATTGCAGCTTCCGATAGAGCTTTTTATTTTTGGATATCAGGAACCAATTTTGAAG
ATTTCTTAAGAAAGTCATTTACATCAGGGACATGAAGAGCAAAGTAGGTATTTTTG
GTCAGTACTTGAATTTGATAGGCTTTATGCAAACAACTCTCCCTCTGCTGGAGTCT
GGCAAGTTTGCTTTTCACTGGACGCTAATTCAAGTGCCATACAAAACTAAAATAAN
AGTTTTACTTATAACACA

Sequence ID 602
CAGAAATCGCAATTGAAGACCAGATTTGTCAAGGTTTGAAACTGACATTTGATACT
ACCTTCTCACCAAACACAGGAAAGAAAAGTGGTAAAATCAAGTCTTCTTACAAGAG
GGAGTGTATAAACCTTGGTTGTGATGTTGACTTTGATTTTGCTGGACCTGCAATCC
ATGGTTCAGCTGTCTTTGGTTATGAGGGCTGGCTTGCTGGCTACCAGATGACCTTT
GACAGTGCCAAATCAAAGCTGACAAGGAATAACTTTGCAGTGGGCTACAGGACTGG
GGACTTCCAGCTACACACTAATGTCAATGATGGGACAGAATTTGGAGGATCAATTT

ATCAGAAAGTTTGTGAAGATCTTGACACTTCAGTAAACCTTGCTTGGACATCAGGT
ACCAACTGCACTCGTTTTGGCATTGCAGCTAAATATCAGTTGGATCCCACTGCTTC
CATTTCTGCAAAAGTCAACAACTCTAGCTTAATTGGAGTAGGCTATACTCAGACTC
TGAGGCCTGGTGTGAAGCTTACACTCTCTGCTCTGGTAGATGGGAAGAGCATTAAT
GCTGGAGGCCACAAGGTTGGGCTCG

Sequence ID - 603 nt: 624
GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGT
CAAAGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTG
CAGTGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGC
ATTGTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGT
AGCCCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCT
TCATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAA
ATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT
TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCA
CATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTA
ATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGA
AGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCCACCCTACCACACAT
TCGAAGAA

Sequence ID - 605 nt: 338
ACCTGAGGCCTCGGTGGGGCCAGTGCGACGCTGGCTTAAGGAGCTGGAGGGGTTCC
TAATACACATTTAATTCAGTTTCTCTTCCCTAAGAGGCTGCCGGAGTTGGGGCCTC
CTCCAGCAGAGACCCTCGGACCCCTGCAGGGCCTGGACTTGGGGTGAACAGGGCTT
CAGTCAGCGCAAGTATTCCATTTGCATTTGGTAATTTTTCATGCCACCTATTTATG
AATATATAAATCTTTATACCAAATCTATTTTTTAAAACATGGAAAAGTTGCCTTTA
TGGAAACTTGGCAGAGCCAGAGTGTACACATTCCTAAACCATTAAACAGATTTCTA
TA

Sequence ID - 606 nt: 556
GGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAGTACTTGAGTGTGCAGCTG
CATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGAAGCTATACCAGTAGGACA
AGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTCTGACTCTCATTTGGAAAC
TGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGAGGGATTTAATGATACTCC
CAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGTGCTCTGAACTCAGTGTTG
GGACTTGAATAAAATTAACCATTGTCATGTTTTCAGAACAACTAAGCTGTTTTATA
TTTCATGTGCATGAAAGCCCTAGAACTAAGTTGTGTTATTTCCAGAAATGAAATAG

ATCCCACAGTTAGATGATGTGGCCATTAGGAAGTACCAAATTTATAAAAATCACTG
GAGGTCTGTCTGAGCAGTACCTAATAAAATATAGTATACTGAAAGTGAACAGATCT
TTGTCTCTTTCTTTGGCTGCTTGATACTTTATCTGTGTCTGCCGGACAGTGC

Sequence ID 607
CAATAAAAGCAGGTTAACCTCAATGATAGCAGTTAAAATGTTCTATCTTATGTATT
TCTTTTAAGTATTACCATTATGGTGCTACTGAGCGTTTTCTTTTGGTAAAAAGAAA
AATGCCATGGGCTGCAGTCTTCTTCCATCACTTTTCCCTACCAGGTCCATTAATAT
GCTTATAACACTAGTGCCAGTTATTTTATTTGATAATGCTTATGGTATTTGTATAT
TTGTTTGCATTCCAATTTTGTTTAATAATGAGTGTGTAAACTGCATACGTTAAATA
AATGTAAATACTAATGTACTGCTGC

Sequence ID 609
TTTTATTACCCAAGTTTTAACCTCTGTCTGGTGATTTGTTGTTGTTGTTGTTGTNG
TTGTTGTTGAAGTTCAGGCTGCATGTGGGATAGGTTTGCTCAGGCATACTTCTTAG
GAAGTAGTCACTTGCATGACTGTTTTTGGGATAACTCTTTGAGTATTTGGAGAGGT
CTATTGTAACTTCTGAAAGGCATTGTTTTTACGTATGAATGTTCTAAAATTCATTC
TAAATGGTCATGAAAAGAAAAGGATTCACATTTTAGAATGGCAATAGTCCCTGAGG
ACTATTATGTCTTTTAGATTTCCTGTGGGTTTCTAGGAATGTTAGTGTAACTTANA
TTTCCACCTACCTGATTTCTGGATGTGCCTATTGGAACTTGCTGAGATCTTTTTTT
TTCCTTAACATGTTGTCCCCTTGACCCGTACTTCGAAACTAAACATATTATTTTAT
TTGCTTACACTTCAGGAGGCAATTGGCAGACACCAGGCCAACAGTCT

Sequence ID 610
GCTCTGACCCCAGTTGGAAATGTATCTGTACTTTGTCCGGCTTCCACTCAAGGACC
ATTTATGACATTGCTTGGTGTCAGCTGACAGGGGCTCTGGCCACAGCTTGTGGGGA
TGACGCGATCCGCGTGTTTCAGGAGGATCCCAACTCGGATCCACAGCAGCCCACCT
TCTCCCTGACAGCCCACTTGCATCAGGCCCATTCCCAGGATGTCAACTGTGTGGCC
TGGAACCCCAAGGAGCCAGGGCTACTGGCCTCCTGCAGTGATGATGGGGAGGTGGC
CTTCTGGAAGTATCAGCGGCCTGAAGGCCTCTGAGCTACCTCGACTTTGGACAGAG
TAATGACTCCCCAGAAAACGTCATATAAGACTTTACCAGCCCCTGAGAGGACCAGG
AGGAGCATCCTTGACCTTCATTTAACTTGGCTCACTTCTCTTCANACTTGGGTAGA
AGTGCAGAGCCACAAAATTGCTTTCCTTCCCCGCCTTTGACATGAGGCCTTCAGTA
AAG

Sequence ID 611
TGCAGGATCCGTCGACT

Sequence ID - 612 nt: 576

GAGAAATATAAGATTATGTATAGATCAAATCTACCTCTATTTGGTGTCCTGAAAGA
GATGAGGAGAATGGGACAAACTTGGAAAGCTTATTTCAAGATAACATTCCTGAGAA
CTTCCCCAATCTTGCTAGAGAGGCCAACATTAAAATTCAGTAAATGCTGAAAACTC
CAGTAAGATATTTCTTAAGAAAATTATTCCCAAGATATATACTCATCAAATTATCT
AAGGTCAAATGAAGGAAAAAATTTTATAGGCAGCTAGAGAGAAATGTCAGGTCACC
TACAAAGAGAATGGCATAAGACAAAAAGTAGAACTCCCAGCAGAAACTCTAAAAGC
CAGAAGAGATTAGGGGCCAATATTTAACATTCTGAAAGAAATTCCAACAAGGAATT
TCATATCCAGCCAAACTAAGCTTCATAATTGAAGGAGAAATAAGATATTTTCCAGA
CAAGCAAATGCTGATGAAATCCATCACCACCAGACCTGCCTTATAAGAGCTCCTGA
GGGAAGCACTAAATATTGAAAGGGAAGAACTTTATGAACCATTTCAAAAACACATT
TAAGTNCACAAAGCAG

Sequence ID - 613 nt: 341

CCTTATTTTACAGGTGAAAAACCACGAATCAGATAGATTTTTATTTGCCCAAGTCA
CATAATATTAAGAACAGGCCAAGTGTGGTGGCTCATGTCTGTAATCTGAGCACTTT
GGGAGGCTAAGGCGGGTGGATTTCCTGAGCCTAGGAGTTTGAGATCAGCCTGGGCA
ACATGGCGAAACCTCATCTCTACAAAACATACAAAAATTAGTCAGTGTGGTGGTGA
GAGCCTGTAGTCCTGGCTACTCGTGAGGCTGAGGTGGGAGCATCACCTGAGCCTGG
GAAGTCGAGGCTGCAGTGGCAACAGAATGGGTAACCTGGACATCAGAGTGAGACCC
TGTCT

Sequence ID 614

CTCACACCTGTAATTCCATTACTTTGGAAGGCTGAGAGAGGAGGATCAGTGGAGCC
CAGGAGTTTGAGACCAGCCTGGGCAATATAGGGAGACCCTGTCTCTACAAAAATGA
AATAGCCAGGCGAGGTGGCATGTGCCTGTGGTCCCAGCTACTTGGGAGACTGAGGT
GGAAGGCTGCCTTGAGCCCAGGAGTTCCAGGCTGCAGTGAGCCATCATTATGCCAC
TGCACTCCAACCTGGGAGACAGAGTGAGAGAGACCCTGTCTCAAACAAACAAACCC
AAAATAGGCCAGGCACAGTGACTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA
AATAGGCGGATCATTTGAGGTCAGGAGTTCAAATTCAAGACCAGCCCGGCCAACAT
GGCAAAACCACATCTCTACTACAAATAAAAAATTAGTTGGGTGTGGNGGAGCATTC
CTGTAATCACAGCTATTCAGGAGGCTGAGGCATGANAACCGCTTCA

Sequence ID - 615 nt: 379

TAAATTTAAAACATTTTAATTAGCTGGCATGATGGCATGCACCTGTAGTCCTACCT
ACTTGGGAGGCCAAGGCAGGAAGATTGCTTGAGCCCAGGAGTTTGAGCTTACTGTG
AGCTGTGATCACACCACTGCACTCCAGCCTGGGTGACAAAGGAAGACCGTATTTCT

AAAAAATAAAAAATACAAATACAACTACAAACTAGCACTAGACCAACAGTGACTAT
GTACCATGAACTGAGGAATATTATTAATTCCACCATTTGCATCTGAGGTTAACAAT
ATGTCAATGACTTAAATAACATCATATCTCTGAGAGTAATTTCTCCTATATTTCCA
TGACAAATGTTAGATAATTTTCCATTTTTTCCATTCAACAAAA

Sequence ID 617
TTTTCAGGCATGTCAGAGAAGGGAGGACTCACTAGAATTAGCAAACAAAACCACCC
TGACATCCTCCTTCAGGAACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGGCG
CATACCCGAGACGATTGTATGAAGAAAATATGGAGGAACTGTTACATGTTCGGTAC
TAAGTCATTTTCAGGGGATTGAAAGACTATTGCTGGATTTCATGATGCTGACTGGC
GTTAGCTGATTAACCCATGTAAATAGGCACTTAAATAGAAGCAGGAAAGGGAGACA
AAGACTGGCTTCTGGACTTCCTCCCTGATCCCCACTCTTACTCATCACCTGCAGTG
GCCAGAATTAGGGACTCAGAATCAAACCAGTGTAAGGCAGTGCTGGCTGCCATTGC
CTGGTCACATTGAAATTGGTGGCTTCATT

Sequence ID - 618 nt: 598
GATTAACTTTCATTTTAAGCTCTTCTCTACTAATTCTGTTCGTATGTTTATTCATT
TTGCGTTGATCATATTTTGTACACCAGGCACTCTTCTCAGTTTTATATGTGTGTTA
ATTTACTCCTTTCAAGAGCCCTATGATACATGAATTTATCTCCATTTTATAGATGA
GGAAATTAAGACCTAGAGTTACTGAACTTGCCCAAGGTTATACAGCTGATGGGTAG
GGCCAGAACTTTGCCTCAGAGAATCTGAATTTCCAAAAAATAACCTAAAAGAGAAA
TTTAAGTACTAATTAGTAAGCAAAGAAATGCACATTTAAGGAAGACAGTGCACATT
TAAGGAAGACAGTAACCTTTTATCTATTAGAGAAAAACACACATTCTGTCTTTAAC
ACACACATAAATCTTATATTGGCAGGGATTTTCTTTATTCAGCAATTATTTATTGG
TTGTCTGCTTTGTGGTACACATAAATGCTGGGGATAAACACTTAATAAAATATACT
TCCTTCTCTTGAATATCTTGCACTTTAAGTGGGAAGGTAAGTCAACAGAGTAGAGG
TGATATATCCAAGTGATAGACTGTTTCATTGCCAGTAG

Sequence ID 619
GTTGCCTGAGAGTGACCTTTGCATCTGCCTGTCCAGCCAGCATGGAACCAAAGCGG
ATCAGAGAGGGCTACCTTGTGAAGAAGGGGAGCGTGTTCAATACGTGGAAACCCAT
GTGGGTTGTATTGTTAGAAGATGGAATTGAATTCTATAAGAAGAAAAGTGACAACA
GCCCCAAAGGAATGATCCCGCTGAAAGGGAGCACTCTGACTAGCCCTTGTCAAGAC
TTTGGCAAAAGGATGTTTGTGTTTAAGATCACTATGACCAAACAGCAGGACCACTT
CTTCCAGGCAGCCTTCCTGGAGGAGAGAGATGCCTGGGTTCGGATATCAATAAGG
CCATTAAATGCATTGAAGGAGGCCAGAAATTTGCCAGGAAATCTACCAGGAGGTCC
ATTCGACTGCCAGAAACCATTGACTTAGGTGCCTTATATTTGTCCATGAAAGACAC

TGAAAAAGGAATAAAAGAACTGAAT

Sequence ID 621

TGGTACTGAACCTACGAGTACACCGACTACGGCGGACTAATCTTCAACTCCTACAT
ACTTCCCCCATTATTCCTAGAACCAGGCGACCTGCGACTCCTTGACGTTGACAATC
GAGTAGTACTCCCGATTGAAGCCCCCATTCGTATAATAATTACATCACAAGACGTC
TTGCACTCATGAGCTGTCCCCACATTAGGCTTAAAAACAGATGCAATTCCCGGACG
TCTAAACCAAACCACTTTCACCGCTACACGACCGGGGGTATACTACGGTCAATGCT
CTGAAATCTGTGGAGCAAACCACAGTTTCATGCCCATCGTCCTAGAATTAATTCCC
CTAAAAATCTTTGAAATAGGGCCCGTATTTACCCTATAGCACCCCCTCTACCCCCT

Sequence ID 622

TTTTTCTTGTTTTTGTGTGTCTACCTTGGCATATACTAAAGGAAGGTGTGTATTCA
TTTATTACATGATATCTCTGGGTTATAATTATTTACATATATGAATTTGAAAGAAA
GATTGAGAGGGATATGTGTGACCTTTGTTTCATTATGATCATTTACATGACTAAAG
ATAAAGATCATATGTCTGATTTTCAGTTTAATGGCAAGTTACTTAAAATAAATGAA
ATATGTTTTTATTGTTTTCGTGGGTTTGATGCTTTGTGTTTTATTTCAAGTAACTT
GAGAATGCATTGTGTTTGGTACTGTTTTTTATGAATATCATTAAAAATTTATTTAA
GGAGAGAGTAATTTTGCAATAATATTTTTGATTTATTTGAAAATAAAATTCAAGAT
AAATGAAATAATTGAAATTTTCTAAAGAAGGAATTGAATATATTTTTACATTTGAA
TGAACTAAGGATTAACTGAACCATTTATATATAGTACTTTCAGAACTGAATGTCTT
AAATGATAAAGCTCTAATTGGTTAAAGTGACTTTCTTTCAAGTCAAAGAACCCAGA
AACTGAATAGATGATCTAACTACTGCCACTGAGGTTTTGGATTAGTGAGTATAAAT
TT

Sequence ID 624

TGCAGGATCCGTCGACT

Sequence ID 625

GACAATCAGAGCAGATCTTGGGCTTCTGTGGCTCATCTCAGCCCTTTATAACTGGC
CTGAGAAGAGGGTTTATCTACTTGTGCAAGTGGCCCAGAAATCTCACTCGTACATG
AGGCTTTGGAACATCCTTGCAAAGGTACGCTGAAAGCAAATTGCTGTTTTCCTGGT
GGTTCTGCACGTTTCCTAACTTTTATCATAGTTTGATTTTCATTATTTAAGAAAAA
ATAAAAAATCCAAAGACCATAAGATGGCATTAGATTTTTTACCATTAAATTATTAA
TGCCTATTTGGTGCTCATAAAGATTAATCATGTCACGCATGTTTCCAATCTTTCTT
TTGCAGTATATTATTTTCTAAAAATTGTTACATGCAAATTTAAACCAAGATTTATC
AGTA

Sequence ID 626

TTGGAAGAAATAAACCAAGGCAGAAAAATTTTAAATGGCCAAAATAAATTGTATTG
CTAACTTAGATGGCCACAGATGGGGGCAGGGGTGGAGAGAGGAGAAATTGAAAACN
CCACAAAGACCCCGCAATGGCTAGAACTTGAAATCTCTGGATATTGCAACAATAGC
AGCCTCCTTAAGTCAGCAAAAAGATAAAGATTGATCCAATGTTCTATATTACAGAA
CAGAGCAGATTGTCAATATAGCAAATAAAGTTACCGTTGAGTGGACTGCGCTGTNT
AAGCTGCTTGGTTGGCCTTAAGTGCCGACAATTAAGAGATGAAGGCAATGAGAACT
GAAACAAACATTTAAGTTCAAGACCCAGTTTACTGACACTGGGACTATTACTATAT
CTCTTTGGGCCTCAGTTTACTTATCTGTAACATTAAGAGGTTGGATTACATGATGT
CTCACGATTCTTTTTTTTATTTAGAGATGGGGTTTTGCTCTGTTGCCCAGGCTGG
AGTGCAGTGGCATGATCATAGCTCACAGCAG

Sequence ID 627

CCAGCCTGTCACTGGCCTGGCCAAGGAGGAGAGACAGGCCAGGGATTCTGGTCCTA
ACTCTACTGGCCACACTGTGTGGCCTGAGACCCCCCTTTCCCTCCCAAGCCCCTGC
CTCCGCATCTGCGTGGTGAAGGCCATTGGCCCTCATCGGTGGATCTGCGTTTCCTC
GGGCCTACACTGTCTAGGATTGTGCGGGGCTGGTGAGAGAACAAGATCTCTTCCGT
GTTCAAGGCAGACTTCCTGCCCCCTGCACCCTGCTCTCTCCCAGGCCTTGAGGTCA
GTGTGAGCCCCAAGGGCAAGAACACTTCTGGAAGGGAGAGTGGATTTGGCTGGGCC
ATCTGGATGGAAGGTAAAAAAAAGAAAATCCCTTGAAAGGAGATTGAGGGAAGTTT

Sequence ID - 628 nt: 419

AAGAGAAAGGACTCAGTGTGTGATCCGGTTTCTTTTTGCTCGCCCCTGTTTTTTGT
AGAATCTCTTCATGCTTGACATACCTACCAGTATTATTCCCGACGACACATATACA
TATGAGAATATACCTTATTTATTTTTGTGTAGGTGTCTGCCTTCACAAATGTCATT
GTCTACTCCTAGAAGAACCAAATACCTCAATTTTTGTTTTTGAGTACTGTACTATC
CTGTAAATATATCTTAAGCAGGTTTGTTTTCAGCACTGATGGAAAATACCAGTGTT
GGGTTTTTTTTTAGTTGCCAACAGTTGTATGTTTGCTGATTATTTATGACCTGAAA
TAATATATTTCTTCTTCTAAGAAGACATTTTGTTACATAAGGATGACTTTTTTATA
CAATGGGAATAAATTATGGCATTTTTT

Sequence ID 629

CTGAGAGTCACTGTGTTTTTAGCCAAATCTAAGGGAGAAAATGAATATTGATAGCA
GCATGCTGTAGCCAGCTCCTTAAAGGAAGGATGGTGCCTGGTACAGAGTTAGAGTT
AGTGCTTCAGTAAATAATGAATGTGTGCTAGGTAGGTTCTGCTGGGTAGGCTGCAT
GCATTGACCAATTTATTCCTCCTTGTTTCAAAACAGGATTTAAGGGCACTTATATA
TATATATTTTTTAGTTTTTTTAATGTAAATGAGAGAATAAAGATATATATATATATGT

CTATATATGTATATATGTATATATATGTCTATATGTCTATATGTATATATGTCTAT
ATGTATATATGTGTGTGTGTATATATATATATATATATAAGTTTTCTGTTGCTA
GCATAACAAACTACCAGAAACTTAGCAACTGAAACAACATGAATTTATCTTACGGT
TCTATAGTTCAGAAGTCTAACGTGTCACTGGGATGAAATCCAGGTTTCAACAGGAC
TGGGTTCCCTTCTAGCTCATTCAGCTACCTGGCTCATTCAGGTTGTNGGCAGAATA
TACTTCCATGAAACTGTAGGGCTGAGACCCCGTTCCTTCCTGGCTATCATCTGAAA
ACTTTC

Sequence ID 630

AGGCGCAGCCCAGCCTCGAAATGCAGAACGACGCCGGCGAGTTCGTGGACCTGTAC
GTGCCGCGGAAATGCTCCGCTAGCAATCGCATCATCGGTGCCAAGGACCACGCATC
CATCCAGATGAACGTGGCCGAGGTTGACAAGGTCACAGGCAGGTTTAATGGCCAGT
TTAAAACTTATGCTATCTGCGGGGCCATTCGTAGGATGGGTGAGTCAGATGATTCC
ATTCTCCGATTGGCCAAGGCCGATGGCATCGTCTCAAAGAACTTTTGACTGGAGAG
AATCACAGATGTGGAATATTTGTCATAAATAAATAATGAAAACCTAAAAAAAAAAA
AAAAAAAAAAAAAA

Sequence ID 631

TNCACTCACACACTCCCAAACCTTAACAAACACATACATGTGCAGCCAACCCAATG
GGCCAGCCTCTTTTATGCTCCTCACATGTTTCCTTTAACTGGAATACCCATGACAG
CTCCCTACATAGTTACTTGTAAACTCCTCCTCTCTGTATAAGTTTTCCTGAATTTT
TTTGATAAAATTAAGTTGTGCCACCCCTTTATGCTCTCTTANAACTTTGTTCTGTT
CTCATGGCTGTTCTGCAACGAATCTCATTGTGTTCTCCTACTCAATTACATTCCTG
CGTCTCCCACTAGATGGCAGACTCTTTGAGAGTAGGAGATTCCCTTGTTATCTCTG
GATCCCTGGCACTTGCAGAAAGCCTGTTACGTAATAATTGCTCAACAATTAGTTTT
TAAATAAATGAATTATTTTTAAAACGCCAAAATTACAATGATTGTGCATTAAGTGA
AAGATGACCATCTAAAAACATAAAGCCATGCTTCATGACATTGGC

Sequence ID 632

GACCATTCAGGGAAATTTTATAAAAAATGCAGATACTGTCTTGAGCAGATCGAAAT
GCCGATGAGGTGGATGCAATTTCCTTTTGTGCAAGCAGTGCACGGTGCCCCCCCCT
CGGGTGTCCGTGCTGTGCCTTAGCTTCCCCAGGTGCCGGGACTCACACCTGCTAGG
GGCTGGGCAAGGCCCCGGCTCTGCTTTCTCTGAAGGGCTTGTCCAAGTTCATTGCC
CTGTTACAGGTGGTCAAGACGTCCGGCCGCCTTGACCCAGGCTACCCTTAGCCAAT
ATCCTCTGCCCCTGGGTGGTTGGTGGCTGGGCCTCAGGGTGGGCAACGTTAGGGGT
TTGGCGAAAGCCCGCCCCATGGGATTGAGGGACGGGGCTGCACTCCAACCGTCTGC
ACCTGCTCTTCCCCCACCCCTGTGGGACCTCATCTTCACGTGCCATGTGTGCTGAA

GGCCCAGGGCCCAGCAGGGGGCAGTGGCACCTGTTGACGGAAAAGCCGAGGTGCTT
ACCAATGGACCTTCTGGCCCGCCCTCCCCTGTACTTGTCGGGCATTCAGGGCCCCG
ACCTGTGCCTACCCGCA

Sequence ID 633
CAACTGTGTTCACTAGCAACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGG
AGAAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGT
GAGGCCCTGGGCAGGCTGCTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTC
CTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC
ATGGCAAGAAAGTGCTCGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTC
AAGGGCACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCACGTGGATCC
TGAGAACTTCAGGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTG
GCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCANAAAGTGGTGGCTGGTGTG
GGCTAATGCCTGGCCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTC
TATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAA
GGGCCTTG

Sequence ID - 634 nt: 511
TTTTTTAATTTCACCAAAATTTGTTGACGTCCCTTGATTTGCTGATAGGGACAATA
ATTAAATATTTTCCACTTGTTTTTATAAAAACTGTAATGGTGATTTGTTTAACAGA
TGTTGACTTAGCACCTTCTCTCTTTTTTTTTTTTTTTTTTTGAGTTGGAGTCTTGC
TCTGTCACCCAGCTGGAGTGCAGTGGCACGATTTCGGCTCACTGCAACCTCCGCCT
CCCAGGTTCGGGCGCTTCTCCTGCCTCAGCCTCCCANATAGTTGGGATTACAGGTG
CATGCCGCCACNCCTAGCTAATGTTTTTTGTATCTTGGTANANATGGNGTTTCACC
TTGTTGCCCATGCCGCTCTTGAACTCCTTGGCCTCCCAAAGTGTTAGGATTACAGG
CGTGAGCCACTGTGCCTGGCCCCAATTTANCACCTTACTGGGTGCTGAGGCTGTGA
GCCATAGTAGAATGCATGTGATCCAGGGCCTTGCTGAATTCATGGGCTAATAGGGA
GCCTGAC

Sequence ID - 635 nt: 592
TGAGCGTTGGGCTGTAGGTCGCTGTGCTGTGTGATCCCCCAGAGCCATGCCCGAGA
TAGTGGATACCTGTTCGTTGGCCTCTCCGGCTTCCGTCTGCCGGACCAAGCACCTG
CACCTGCGCTGCAGCGTCGACTTTACTCGCCGGACGCTGACCGGGACTGCTGCTCT
CACGGTCCAGTCTCAGGAGGACAATCTGCGCAGCCTGGTTTTGGATACAAAGGACC
TTACAATAGAAAAAGTAGTGATCAATGGACAAGAAGTCAAATATGCTCTTGGAGAA
AGACAAAGTTACAAGGGATCGCCAATGGAAATCTCTCTTCCTATCGCTTTGAGCAA
AAATCAAGAAATTGTTATAGAAATTTCTTTTGAGACCTCTCCAAAATCTTCTGCTC

TCCAGTGGCTCACTCCTGAACAGACTTCTGGGAAGGAACACCCATATCTCTTTAGT
CAGTGCCAGGCCATCCACTGCAGAGCAATCCTTCCTTGTCAGGACACTCCTTCTGN
GAAATTAACCTATACTGCAGAGGTGTCTGTCCCTAAAGAACTGGTGGCACTTATGA
GTGCTATTCGTGATGGAGAAACACCTGACCCA

Sequence ID - 636 nt: 572
CTTANAAGAGTTGCTCATTCACACCCACGCCCTTGCCCAAGGCTGGCCCACTCAGA
GCGAAACTTAACTTTTGTCTGGATGGGAAGAGAAGTAAGTCTACCCCGAGGTTGCC
ATGTTGAAGAGTGAGAGGTCCAAGTGATTCTGTGCATTGAAACCAAGACACCCCAC
CCAGAACACTTCTTCCCTCCCTCAGCCCAAACCAAAGGCTGGGGTTCTCATCTCCA
AGTGGCTGTTCTCCAACTTTCCCAAGCCGCTTGCATTCCCCAGACTGGACTACTGT
GGCGGTTAGGTTAGATTTGAAGACGGGGCCCAGGCTGGGTATGAACGGGTGCAGCC
CTCTTCTCCTCTTCCCCCCCACATCTCTCATGAGAGAGGTAGTGGCATTTCCTTCT
CAGGGAGCTTCAATGGGAAAGGTCTCGAAAGCTTCAGGAGGAGCAGAATACCAACG
CAGGGGGATGGCTGTAACGATCTCACCGTCTCCTAACCTCAGTCCCTTTTTTGAGA
GTGAATGGTGGAGGGTGGGAAAGGGACCCAAATTTGTAGATCTCTTTGTCTGGGGG
AGGGGAANGATG

Sequence ID - 637 nt: 482
TTAAAACAGGCGCAGGGGTAAAAATGAGAATGAATCTGAAAAAAGAGAGTTGGTGT
TTAAAGAGGATGGACAAGAGTATGCTCAGGTAATCAAAATGTTGGGAAATGGACGA
TTGGAAGCATTGTGTTTTGATGGTGTAAAGAGGTTATGCCATATCAGAGGGAAATT
GAGAAAAAAGGTTTGGATAAATACATCAGACATTATATTGGTTGGTCTACGGGACT
ATCAGGATAACAAAGCTGATGTAATTTTAAAGTACAATGCAGATGAAGCTAGAAGC
CTGAAGGCATATGGCGAGCTTCCAGAACATGCTAAAATCAATGAAACAGACACATT
TGGTCCTGGAGATGATGATGAAATCCAGTTTGACGATATTGGAGATGATGATGAAG
ACATTGATGATATCTAAATTGAACCAAGTGTTTTTACATGACAAGTTCTCTGAGGA
TGGTTCTACAGTTGGGATTTTGGCCATCATCAAC

Sequence ID - 638 nt: 545
TTTGAAGGCAAAGAGGGATTAATCTGTGCTGGCATCATGTAAGGAGACTTGATAGA
TAAGAAAAAGCTTTACCTAAGTTTTGAAGAATAGGTTTTTCATAATGGAAAATTTA
AGGGAAAAAATCTCCAAAAAAGTGCTACTCAAGTTTTATCCATTTGTATTTCCAACA
CAGCCTAGGACAGTACCTGCACATAGTAGGTGATTAATAAAAATTTAGAAAGCATT
AATACTAAAGAGGAAAAATAGCAATGGCAAGAAAACACATGTAGGGAACACATGTA
GCCAAAAAATAATATATAATCAGAGAAATAATAGGACTTCTGGAAAAAAAAGATGA
GATCAGATTGGTTAGGATCTTTACTAACATGACAAGAGCATGAATTTTTTTTCTGT

AGATAATAAGTATGAAAGAATTTTAGCTTAAAAATTAGCATAATTTGGATCCACAT
ATGCAAATCAATGAATGTAATTCATAATATAAACAGAACTAAACACAAAAACCACG
TGATTATCTCAATAGACACAGAAAAGGCCTTCAAAAAAATT

Sequence ID - 639 nt: 624
GACACACGAGCATATTTCACCTCCGCTACCATAATCATCGCTATCCCCACCGGCGT
CAAAGTATTTAGCTGACTCGCCACACTCCACGGAAGCAATATGAAATGATCTGCTG
CAGTGCTCTGAGCCCTAGGATTCATCTTTCTTTTCACCGTAGGTGGCCTGACTGGC
ATTGTATTAGCAAACTCATCACTAGACATCGTACTACACGACACGTACTACGTTGT
AGCCCACTTCCACTATGTCCTATCAATAGGAGCTGTATTTGCCATCATAGGAGGCT
TCATTCACTGATTTCCCCTATTCTCAGGCTACACCCTAGACCAAACCTACGCCAAA
ATCCATTTCACTATCATATTCATCGGCGTAAATCTAACTTTCTTCCCACAACACTT
TCTCGGCCTATCCGGAATGCCCCGACGTTACTCGGACTACCCCGATGCATACACCA
CATGAAACATCCTATCATCTGTAGGCTCATTCATTTCTCTAACAGCAGTAATATTA
ATAATTTTCATGATTTGAGAAGCCTTCGCTTCGAAGCGAAAAGTCCTAATAGTAGA
AGAACCCTCCATAAACCTGGAGTGACTATATGGATGCCCCCCACCCTACCACACAT
TCGAAGAA

Sequence ID 641
CAAGATGACAAAGAAAAGAAGGAACAATGGTCGTGCCAAAAAGGGCCGCGGCCACG
TGCAGCCTATTCGCTGCACTAACTGTGCCCGATGCGTGCCCAAGGACAAGGCCATT
AAGAAATTCGTCATTCGAAACATAGTGGAGGCCGCAGCAGTCAGGGACATTTCTGA
AGCGAGCGTCTTCGATGCCTATGTGCTTCCCAAGCTGTATGTGAAGCTACATTACT
GTGTGAGTTGTGCAATTCACAGCAAAGTAGTCAGGAATCGATCTCGTGAAGCCCGC
AAGGACCGAACACCCCCACCCCGATTTAGACCTGCGGGTGCTGCCCCACGTCCCCC
ACCAAAGCCCATGTAAGGAGCTGAGTTCTTAAAGACTGAAGACAGGCTATTCTCTG
GAGAAAAATAAAATGGAAATTGTACTTAA

Sequence ID 642
TGCTTGGCCCTCTACCTCCTGCCCTCTTCCTGTTCATCTCCCAACCACTGCACTCT
TGATTTTTATACCACACAGAAGGTAAGAAAATTCTAGGAACCCTAAGGATCAATCC
TCTCCATTTTCACTCAAATGCCTGGGGCCCAGCTCTGCAATGACTGACTCCAGGGC
CTCTTTCCTCACTGCCAGCATAGAAGTCAGGGGAGCCAGCTGGGCCCTGCGGTCAG
GAAGGTTCTCATTTTTGGAGCATTCCCTGAGCCCAGATCATAGGAGCAGCTGTCCC
TGGTGGGACACAGGAGTCATGACTCCTACCCTCCACCCTCCACACCCACCAGGCAT
TTAGCAGTCTGTCCTATGCAAGACAGATGAATTCTCAGCCAGGATACCTCAAGGCA
GGCAAAGGTGAGTGGAGGGAAAATTCACAAACATTCAGGGTGTGTGGTGCTGGCAT

CACCATGGCCAAATCCAAGAGGTCTTCCTGGAAGAGGGCCCAAACTGGAACCAAAA
GAATGCTGTCAGCAGTTGGAATAGAGCTGTGAATT

Sequence ID 643

CTTTCCAAGAGGAATCCTCGGCAGATAAACTGGACTGTCCTCTACAGAAGGAAGCA
CAAAAAGGGACAGTCGGAAGAAATTCAAAAGAAAAGAACCCGCCGAGCAGTCAAAT
TCCAGAGGGCCATTACTGGTGCATCTCTTGCTGATATAATGGCCAAGAGGAATCAG
AAACCTGAAGTTAGAAAGGCTCAACGAGAACAAGCTATCAGGGCTGCTAAGGAAGC
AAAAAAGGCTAAGCAAGCATCTAAAAAGACTGCAATGGCTGCTGCTAAGGCACCTA
CAAAGGCAGCACCTAAGCAAAAGATTGTGAAGCCTGTGAAAGTTTCAGCTCCCCGA
GTTGGTGGAAAACGCTAAACTGGCAGATTAGATTTTTAAATAAAGATTGGATTATA
ACTCT

Sequence ID 644

CTTTGATAGAGAAGAAAATTCTCCTAGGATACAAGAGCCTCAACATTTTAAAGATT
TTCTGCATCTCAAAAGCGTAGGCTCCTTGCTGGGCAAGGTGAGCCTCTGTGAGTCC
TCATAGGACCGAGCAAATCTGATTCACCCCAGAAAATCCAATATCGAAGCTGAGCT
TTGGCCTGAGCGGGTTCCATTTCCTCCCCAGATCCTATTTAGGAAGTGTCTCCTGA
CAACCTCCAAAAGGTGCTAACATGCAACGTTCTGAAGGGTTATTGCTCAAAAACAA
GATTTTCCTTGTGGTCAAGACTCTGCGAGCCTCGAACACGATGAATCCGCTCGAAT
GGGCTTGGGCTTTGCCCGGGTGGCGCACGCTCACACGCTGGAAGCACAGCTTTGAC
GATCTCCACACACGCACAGGCACACACGCCACAGATGATGCCGGCTCATTCTCAGG
GGGTGTCTAAGTTCTGCTTTAAATATTTACCCCCTAATTGTACAAACAATAGGGGC
ATGAGCCTGGTACTCGATAAATGGGGACTTNCTTAAAA

Sequence ID - 645 nt: 649

CTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTCGT
CCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTG
CCCGGGGTGCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAA
CACCGAGTTCAAGAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATG
ACCGCTTCGCCAACTACATCGACAAGGTGCGCTTCCTGGAGCAGCAGAATAAGATC
CTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCT
CTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACA
AAGCCCGCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGG
GAGAAATTGCAGGAGGAGATGCTTCAGAGAGAGGAAGCCGAAAACACCCTGCAATC
TTTCAGACAGGAAATCCAGGAGCTGCAGGCTCAGATTCAGGAACAGCATGTCCAAA

TCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCTTGCGTGACGTACGTANC
AATATGAAAGTGTGGCTGCCAAAAACCTTGCAG

Sequence ID - 646 nt: 600

GAGATGTCTCGCTCCGTGGCCTTAGCTGTGCTCGCGCTACTCTCTCTTTCTGGCCT
GGAGGCTATCCAGCGTACTCCAAAGATTCAGGTTTACTCACGTCATCCAGCAGAGA
ATGGAAAGTCAAATTTCCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGACATT
GAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAGACTT
GTCTTTCAGCAAGGACTGGTCTTTCTATCTCTTGTACTACACTGAATTCACCCCCA
CTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTCACAGCCCAAG
ATAGTTAAGTGGGATCGAGACATGTAAGCAGCATCATGGAGGTTTGAAGATGCCGC
ATTTGGATTGGATGAATTCCAAATTCTGCTTGCTTGCTTTTTAATATTGATATGCT
TATACACTTACACTTTATGCACAAAATGTAGGGTTATAATAATGTTAACATGGACA
TGATCTTCTTTATAATTCTACTTTGAGTGCTGTCTCCATGTTTGATGTATCTGAGC
AGGGTGCTCCACAGGTAGCTCTAGGAGGGCTGGCAACTTA

Sequence ID 647

CGAATGTGCAGGTTTGTTACATAGGTATATATATGCCATGATGGAAATATTTATTT
TTTTAAGCGTAATTTTGCCAAATAATAAAAACAGAAGGAAATTGAGATTAGAGGGA
GGTGTTTAAAGAGAGGTTATAGAGTAGAAGATTTGATGCTGGAGAGGTTAAGGTGC
AATAAGAATTTAGGGAGAAATGTTGTTCATTATTGGAGGGTAAATGATGTGGTGCC
TGAGGTCTGTACGTTACCTCTTAACAATTTCTGTCCTTCAGATGGAAACTCTTTAA
CTTCTCGTAAAAGTCATATACCTATATAATAAAGCTACTGATTTCCAAAAA

Sequence ID 648

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID - 649 nt: 425

CAAAAAAACGAAGAAAAGTGACGACAGTCTGAGGGACTTATGGGAGATCATCAAGT
GAACCACTATATGTGTAATGTAAGTCTTGGAATGAGAAGAGAGAAGGAGAAGGAGG
AGAGAGCTTATTTGTAGAAATAATGGCTGAAAACATCCCAAACTTTCCTTTTTTTG
AGGAAAGAAATAGGCATACAAGTTCAAGAAACTCAAGGAACTCCAGAGAGGACAAT
TCTAAAGACACCCCCTCTAACATACATTATAATCAAATTGTCAAAAGTAAAATACA
AAGAGAATCTTTTAAATTGACAAGAGAAAAGCAGCTGGTCACGTTCAAGGGAGTTC
TATAAGAATTTCAGCAGATTTCTCAGCAGAAACCTTGCAGGCCAACAGGCAGTGGG
ATGATACATTCAAAGTGCAAAAAAAAAAAAAA

Sequence ID 650

CGAGAGTTTACCAGTNGCCTAATAATGCAATAAAAAATGCTTTGAGATAGCTAACN
GCCCATAAAACAAACTCAAATTGCTTATAAAGTTTCTTCCCATGTTCCCATTTGAT
GAAAAGTCTTACATCACATATAACTGGGAAGCAGGGGTCCCTCCTCAATTTTCAGA
CATTTTGAAAGGATGACAGTTCTGTTTGTTAGATGAGTAAACCTCTATATTCATAA
GTTCTAAAATCCTTCATTATGAGGGATTCAAAGTATTTATAAAAACACTGCCCTCT
AAAAATTTCCTCAGATCTGAAGTATGGNCTTGGNCCTGAATATACAGTGTTATCCT
ATGTTTAAAAGGGTGATCCAGACATGAGACGCAACTAGTTGGTGCATAAGAAGGCC
CCACTTGGCTATTTCATATCTACCTACAATTGACCAAAAAAAATTTTTTAGGCCAG
CAATTATTATTTAGCTTCGCTCTTTCTAGTGCAAGAAACTGCAGGCTGGATCAGTA
GTTCAACAGCTAAACAGTCATAAAATAGTCATTGGCATGTTAAATTTCTTTCAATG
CTTCAAAGATAAATTCCAATTCTATTTACTTATTCATTGNGACNGNATTACTAAAC
AGGTAAGGATGGGAATA

Sequence ID - 651 nt: 251

CTTTGGGAGGCCGAGGCGGGCGGATCACTTGAGGTCAGGGGTTCGAGACCAGTCTG
GCCAACATGGTGAAACCCCAACTCTACTAAAAATACAAAAGTTAGCCAAGTGTGGT
GGCAAGTGCCTGTAATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATCACTTTGA
ACCTGGGAGGCGGAGGTTGCAGTGAGCCAAGATCGTGCCACTGCACTTCAGCCTGG
GCAACAGAGCAAGATTCCGTCCATCTC

Sequence ID 652

CTTTCTTCAGCCTTGCAGACACCTAAACATCATGTAATTACCTAAGGAATTCCCAA
GTGCCTCTTCCAGGTTATACGTGTAAATAGCTGTTTTTATGCAAGATTAGTTAGAT
ACTGCTCTTTACAGGATGAGTGGTGTTGTCTTTGGCTGGGGGGGNCTTAAATGTGT
TTCTAATGTGTGTGTCAAATAATTACCTGTTAAACAGACTGCCAATCTGGCTGAAG
CCAATGCTTCTGAAGAAGATAAAATTAAAGCAATGATGTCGCAATCTGGCCATGAA
TACGACCCAATCAATTACATGAAGAAACCTCTAGGTCCACCACCTCCATCTTACAC
GTGTTTCCGTTGTGGTAAACCTGGACATTATATTAAGAATTGCCCAACAAATGGGG
ATAAAAACTTTGAATCTGGTCCTAGGATTAAAAAGAGCACTGGAATTCCCAGAAGT
TTCATGATGGAAGTGAAAGATCCTAATATGAAAGGTGCAATGCTTACCAACACTGG
AAAATATGCAATCCAACTATAGATGCAGAAGCATATGCAATTGGGAAGAAAGAGAA
ACCTCCTTNTTACCAGAGAGCCATCTTNTTTCT

Sequence ID 653

GTTGTGACTCGTTGGCATGTGATCTGAAGTTCCTGCCCTGCAGCTGACGAGCCAGT
GTTTCAATAATTAAAAACAACTCAACTCACTGTCCTCCTGCCTTGAATTTGATCAT

TGCGCTTTGCATGTATGTATCACAATACCACATGTACCCCATAAATATGTACAAAG
ATTATGTGTCAATAAAAAACAAAAATTAAAATCCCAATTTTTA

Sequence ID 654
GTTGCTAGTAGCGGCAGGAAGATGTCAGGCTCACTTTCCTCTGATTCCCGAAATGG
GGGGAACCTCTAACCATAAAGGAATGGTAGAACAGTCCATTCCTCGGATCAGAGAA
AAATGCAGACATGGTGTCACCTGGATTTTTTTCTGCCCATGAATGTTGCCAGTCAG
TACCTGTCCTCCTTGTTTCTCTATTTTTGGTTATGAATGTTGGGGTTACCACCTGC
ATTTAGGGGAAAATTGTGTTCTG

Sequence ID 655
GTCCCCGGGAATCGCGGCCGCGTCGACGGTTTATTTTCAGTGCTTGAAGATACATT
CACAAATACTTGGTTTGGGAAGACACCGTTTAATTTTAAGTTAACTTGCATGTTGT
AAATGCGTTTTATGTTTAAATAAAGAGGAAAATTTTTTGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAATTTTT

Sequence ID 656
TAGAGGCCTGAATAGGTAGACAATGGCAGCAGCGTTTTTAATCACAGTCCTATTCA
TGCCCTAATTCGGGAGTGATGATTAAAGGACATTAGAGGGAGCACTTTGACATCTG
ATCCTTTGAACTGACGTCTGTGCAGGCTGCACTCCATAGAGCTCACTTGGCCAAAC
TGATTTCCTTAAATAAAGTGCTGTGATTTCCAATGTAGGAAATATTACATTAGAGC
CTATTGAAATGATTAGGAATTGAGGAGCTTTTCTTTAGGTGGGAATGTGGTGTATG
CTGTATACTCACAAAAGTGAGATCATTAATATTGCATGTACTACTTTGAATATCAG
GGACCACAGAGAAATAGCATGAGAAACGCCTTCCTGCAGTCATGCACTTAAAATGA
ATATGAACAAAAATGTGGAACTCTGCTGTCATAGCTCTCCG

Sequence ID 657
GGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTTTTTT
CTCTTTGAAAGATAGAGATTAATACAACTCTTAAAAAATATAGTCAATAGGTTACT
AAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATTTTAAG
AGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGGTTTCT
AAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTTAAA
AGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAGAAGGGCAAT
GCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTA

Sequence ID 658

GACCTTTGAGAAAATTAATTTAAATCCTAGAACTTTGGGTGAACCGAAGAAATTTA
TAATATTTGTTTAGTTAATAACAGATAAAAAGGAAAGATTCAAGCCTATTGGATGA
GAATTTGTACATTATTTTAGAGCTAATAATAATGGTTTTCAGTTTAGTGAGGATTT
AAAAAATGTTTTTGAATCAAACTTTTTTTCTTTATAATCCTTTTTAACTAACTCAG
GAAATAAGGTATTATGAAATCCACACACTGTTACCTCCTTAAAGTATGAGGATACT
TCCCACTGTTTGGTCCACTAGTGGCTGATTATTTTGTTTGTGGATTATTTGTAATT
TTCTTTTTAATTCTTCCTTAAAGAGCATGGCATTTGGAGTCACAGACCTATATTTG
AATCCTGTCATTTACTAGCGTTTTGACCTTGAACAATTATGCTCAGAGTCTCAGTT
TTTTCTTGTAAAGTGATGATGATACTACTTAACTCACAGGGTTGTAGTGAAGATCA
AATGAGATCATGTCTGTANAACACCCTGCCCGGCACTCAATAAGTATTAATAGGAA
CCCATATACCTC

Sequence ID 660
TGTTTTTATTTTTTAAAAGGTATAAACACCAAAAAAAAAATTAACATTGTATGAAG
ATGGAAAATAAGAAGATGCACTTTCTGTAACTTTGTCTAAGGATTTAAATTACTAA
CTTATGAACTCCAATTTGAATTGAACTTAACTATCGGCTTTCTTACTGGTAAAATT
ATATGGTTTATTTTAAATGCGTACATATTGACCAATGGCCTCTGAAAAAGCACATT
TTAGATACTGAAATTGAAGGAAAGAAAATGCATCTTCAAACATTTTTTGGAATCTC
ACCACATATACTTTGTTANATTTGTGTATTGTAGGGTGTTTGTTTTGTATTTTTGT
ATTGTATATGAACTTTTTTTAAATGTGACAGTTAAACACATCTTTAAAAGCATAGT
CACAGACAAAAGCATACAGTATAAAAATTTCCTTGAAAACTCCTACAATATTATAT
TTGGAGGCAGCTTCAGACTGTTTTATTGG

Seqeunce ID 661
CTCTGGCACACATTAGTTCCTCTTATATTACATTGATATAAGCAAGTCATATGGAT
TTATCTGAGTGTAAGGAGAGCTGGAAAAAATAGTTTCTAGCAGGTCAGCCACCTCC
CAGTGAGGGCTGCATACCATAGAAGGGGAGAATGAATTTTGGGAAAACAGGTAATT
ATCTCTGTCACAGAAGGGGATGAAAAGTATGGTAGTTACNCAAGTTANACATCTGT
ATGGAAAATACCACTTGGTTCTACAAATGNGG

Sequence ID - 663 nt: 627
GCCTCCCGGGTTCAGGGATTTCTCCTGCCTCAGCCTCCTGAGTGGCTGCATTGCAG
GCACCTGCCACCACGCCTTGCAAATTTTTGTGTTTTTAGTGGAGATGGGGTTTTGC
CATGTTGGCCAGGCTGGTCTCGGACTCCTGACCTCAGGTGATCCGCCCGCCTCAGC
CTCCCAGAGGGCTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCCCAAGTTTTGC
ATCTTTTAATGCCCTCTGAACAAATACATAGAGAAAACTCTCAGAACAATTAAAAC
CTGCAGAGCAACAGTGTCCTCCATGTCTTAGGTTTCAAGTTTGCCTCTAAAATTCT

AATCCATATTTTTCTACTTCTCAGATAATTTATGTGTGTGTACTCTTCCTAGACGT
ACAAGAGACTTTTTAATGCTAAATATTTGTCAGTGCTTAACAAAAACTCAATTTCA
CATTACTCATATTGTTTTTGTTTTAATTGAATGTGAATTAAATTTTTATTAGTTAT
TTGATTTGGAATGTTATGTATGCCATTAACACTATTAGGGGAATCTCTAGCATTTC
TGTATTTTTAAAGAATTTGATTCTTTTGTANATTCTGCCTGTGTGGCATTTTAAAC
ATGTGTGACAT

Sequence ID - 665 nt: 345
ACCGGCGACATGGCCAAACGTACCAAGAAAGTCGGGATCGTCGGTAAATACGGGAC
CCGCTATGGGGCGTCCCTCCGGAAAATGGTGAAGAAAATTGAAATCAGCCAGCACG
CCAAGTACACTTGCTCTTTCTGTGGCAAAACCAAGATGAAGAGACGAGCTGTGGGG
ATCTGGCACTGTGGTTCCTGCATGAAGACAGTGGCTGGCGGTGCCTGGACGTACAA
TACCACTTCCGCTGTCACGGTAAAGTCCGCCATCAGAAGACTGAAGGAGTTGAAAG
ACCAGTAGACGCTCCTCTACTCTTTGAGACATCACTGGCCTATAATAAATGGGTTA
ATTTATGTA

Sequence ID - 666 nt: 252
ATAATTCAGAACTTCTTCATATGCTCGAGTCTCCAGAGTCACTCCGTTCTAAGGTT
GATGAAGCTGTAGCTGTACTACAAGCCCACCAAGCTAAAGAGGCTGCCCAGAAAGC
AGTTAACAGTGCCACCGGTGTTCCAACTGTTTAAAATTGATCAGGGACCATGAAAA
GAAACTTGTGCTTCACCGAAGAAAAATATCTAAACATCGAAAAACTTAAATATTAT
GGAAAAAAAACATTGCAAAATATAAAAT

Sequence ID 669
TTACTTTTAACCAGNGAAATTGACCTGCCCGTGAANAGGCGGGCNTGACACAGCAA
GACGAGAAGACCCTATGGAGCTTTAATTTATTAATGCAAACGGTACCTAACAAACC
CACAGGTCCTAAACTACCAAACCTGCATTAAAAATTTCGGTTGGGGCGACCTCGGA
GCAGAACCCAACCTCCGAGCAGTACATGCTAAGACTTCACCAGTCAAAGCGAACTA
CTATACTCAATTGATCCAATAACTTGACCAACGGAACAAGTTACCCTAGGGATAAC
AGCGCAATCCTATT

Sequence ID 670
GGCTGATTCCTGAGCTATAAAAGCATAATTGCTTTATATTTTGGATCATTTTTTAC
TGGGGGCGGACTTGGGGGGGGTTGCATACAAAGATAACATATATATCCAACTTTCT
GAAATGAAATGTTTTTAGATTACTTTTTCAACTGTAAATAATGTACATTTAATGTC
ACAAGAAAAAAATGTCTTCTGCAAATTTTCTAGTATAACAGAAATTTTTGTAGATG
AAAAAAATCATTATGTTTAGAGGTCTAATGCTATGTTTTCATATTACAGAGTGAAT

TTGTATTTAAACAAAAATTTAAATTTTGGAATCCTCTAAACATTTTTGTATCTTTA
ATTGGTTTATTATTAAATAAATCATATAAAAATT

Sequence ID 671

CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCA
GGCCTCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGC
TCTGTCTTTAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTAC
CTGAAAGAAACTACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTAT
TTCAGAACCATTCTACCTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACA
GTACATCCACCCTAACTCTATAAATGTTGATGGTAATACAGCATTATCTATCACCA
ATAACCCTTCAGCACTA

Sequence ID 672

CAGGAAGTCACCTGGGATTGGCTGCCTCACCCACTCACAGTGCCATCCCTGCCCCA
GGCCTCCCAGTGGCAATTCCAAACCTGGGTCCCTCCCTGAGCTCTCTGCCTTCTGC
TCTGTCTTTAATGCTACCAATGGGTATTGGGGATCGAGGGGTGATGTGTGGGTTAC
CTGAAAGAAACTACACCCTACCTCCACCACCTTACCCTCACCTGGAGAGCAGTTAT
TTCANAACCATTCTACCTGGCATTTTATCTTATTTAGCTGACAGACCACCTCCACA
GTACATCCACCCTAACTCTATAAATGTTGATGGTAATACAGCATTATCTATCACCA
ATAACCCTTCAGCACTAGATCCCTATCAGTCCAATGGAAATGTTGGATTANAACCA
GGCATTGTTTCAATANACTCTCGCTCTGTGAACACACATGG

Sequence ID 673

GGGTTTTCTTTCGGAAGCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCGCGTC
GACTGCTAAACAGAATACTGCTATTTTGAGAGAGTCAAGACTCTTTCTTAAGGGCC
AAGAAAGCCACNTGNNCCCTNGGNCTAATCTGGCTGAGTAGTCAGTTATAAAAGCC
NTAATNGCTTNNTNTTTGGNNTCNTTTTTNNCNGGGGNCGGNCTTGGGGGGGGTTG
CNTCCAAAGATANCATNTNTTTCCAACTTTNTNAANNNAANNGTTTTAAAATCCCT
TTTCCNCCNGAAAANANNGCCCTTTAAGNGCCNCAAAAAAAAANNGTNTTCTGCAN
NTTTTCTANTATNACAAANNTTTTNGTAGAANAAAAATTTTTTTTTAGNGGCTACC
CTTTNTTTNTTANNCANNGGAGTTTNTTTTTACAAAAAAAAAANATTGGGNCCCCT
CCACAACCTTGGGTCTNTAATNGGGGGGTTTTTAAATAAANCNTNTNTAAATCCCC
CNNNNNNNNNCNNNNNNNNNCCNNNNNNNNNNNNNNCCCNNNNAAAAAATTTTTNC
TCCCCCNCCCTTTTTCTTCCTGCCGGCCCCAATTTAAGCCCNGGCGCTTGGGGCAA
ATCCCCCTTTAGNGGGGGGGTTTANAAAAACCNGGGGCGGGGNTTTAAAACCNCGG
GGNNNGGGGAA

Sequence ID 674

ACCTCTAGCATCACCAGTATTAGAGGCACCGCCTGCCCAGTGACACATG-TTTAAC
GGCCGCGGTACCCTAACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAATTAGGG
ACCTGTNTGAATGGCTCCACNAGGGTTCACTTGTCTCTTACTTTTAACCAGTGAAA
TTGACCTGCC

Sequence ID - 675 nt: 591

GTATAGAAAATAATGTCCCCAGNGCATAGAAAAAATGAGTCTCTGGGCCAGTGAAT
ACAAAACATCATGTCGAGAATCATTGGAAGATATACAGAGTTCGTATTTCAGCTTT
GTTTATCCTTCCTGTTAAGAGCCTCTGAGTTTTTAGTTTTAAAGGATGAAAAGCT
TATGCAACATGCTCAGCAGGAGCTTCATCAACGATATATGTCAGATCTAAAGGTAT
ATTTTCATTCTGTAATTATGTTACATAAAAGCAATGTAAATCAGAATAAATATGTT
AGACCAGAATAAAATTAATTATATTCTGGTCTTCAAAGGACACACAGAACAGATAT
CAGCAGAATCACTTAATACTTCATAGAACAAAAATCACTCAAAACCTGTTTATAAC
CAAAGAATTCATGAAAAAGAAAGCCTTTGCCATTTGTCTTAGAAAGTTATTTTTTA
AAAAAAAATCATACTTACTATTAGTATCTATGGAAGTATATGTAACAATTTTTATG
TAAAGGTCATCTTTCTGTGATAGTGAAAAAATATGTCTTTACTAAGTTGAAATGAA
TACTTTCTGNCTTTGCTAATGGATAGTTATT

Sequence ID 676

CTCAATTCTACTAAAAAGCCCCCCAAGAAAAGCGAATGAGAAAACAGAGTCATCCT
CTGCACAGCAAGTAGCAGTGTCACGCCTTAGCGCTTCCAGCTCCAGCTCAGATTCC
AGCTCCTCCTCTTCCTCGTCGTCGTCTTCAGACACCAGTGATTCAGACTCAGGCTA
AGGGGTCAGGCCAGATGGGGCAGGAAGGCTNCGCAGGACCGGACCCCTAGACCACC
CTGCCCCACCTGCCCCTTCCCCCTTTGCTGTGACACTTCTTCATCTCACCCCCCCC
TGCCCCCCTCTAGGAGAGCTGGCTCTGCAGTGGGGGAGGGATGCAGGGA

Sequence ID 679

GNANCNTTTCCTNTCGNAAANCGCGCCTTGTGTTGGTACCCGGGAATTCGCGGCCG
CGTCGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAANTNTAGACTCGANCAAGCTT
ATGCANGCNTGCGGCCGCAATTCGAGCTCGGCCGACTTGGCCAATTCGCCCTATAG
NGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGNGACTGGGAAAACC
CTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGT
AATANCGAANAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGG
CGAANGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTA
AATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAA
AAGAATAGACCGAGATAGGGTTGAGNGTTGTTCCAGTTTGGAACAANAGTCCACTN

TTAAAGAACGNGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGG
CCCACTACGTGAACCATCNCCCTAATCAAGTTTTTTGGGGTCGAGGNGCCGTAAAG
CACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCTTGACGGGGAAAGCCC
GGCGAACGTGGCGAAA

Sequence ID 682
CACCTGCAGTCCAAGTACATCGGCACGGGCCACGCCGACACCACCAAGTGGGAGTG
GCTGGTGAACCAACACCGCGACTCGTACTGCTCCTACATGGGCCACTTCGACCTTC
TCAACTACTTCGCCATTGCGGAGAATGAGAGCAAAGCGCGAGTCCGCTTCAACTTG
ATGGAAAAGATGCTTCAGCCTTGTGGACCGCCAGCCGACAAGCCCGAGGAAAACTG
AAACTTTGCTTAACNACCGAATGGNGGGGANCTTTTCCAACGNTTTT

Sequence ID 683
TTGGTTTCATACTGNTGGGGNTTGAATGNTCCCTNCAACACTNATGTTGANACTTA
ATCCCTAATGNGGCAATACTGAAAGGTGGGGCCTTTGAGATGTGATTGGATCGTAA
GGCTGTGCCTTCATTCATGGGTTAATGGATTAATGGGTTATCACAGGAATGGGACT
GGTGGCTTTATAAGAAGAGGAAAAGAGAACTGAGCTTGCATGCCC

Sequence ID - 684 nt: 545
GTGGAAGNGACATCGTCTTTAAACCCTGCGTGGCAATCCCTGACGCACCGCCGTGA
TGCCCANGGAAGACAGGGCGACCTGGAAGTCCAACTACTTCCTTAAGATCATCCAA
CTATTGGATGATTATCCGAAATGTTTCATTGTGGGAGCAGACAATGTGGGCTCCAA
GCAGATGCAGCAGATCCGCATGTCCCTTCNCGGGAAGGCTGTGGTGCTGATGGGCA
AGAACACCATGATGCGCAAGGCCATCCGAGGGCACCTGGAAAACAACCCAGCTCTG
GAGAAACTGCTGCCTCATATCCGGGGGAATGTGGGCTTTGTGTTCACCAAGGAGGA
CCTCACTGANATCAGGGACATGTTGCTGGCCAATAAGGTGCCAGCTGCTGCCCGTG
CTGGTGCCATTGCCCCATGTGAAGTCACTGTGCCAGCCCAGAACACTGGTCTCGGG
CCCGATAAGACCTCCTTTTTCCAGGCTTTAGGTATCACCACTAAAATCTCCAGGGG
CACCATTGAAATCCTGAGTGATGTGCACTGATCAAGACTGG

Sequence ID 685
GGAAAGGGCCATTTTATTGCCTAAAACCACCTGGNTTTTNAGGTAACAGTTCCAAC
ATGTCCTTTTTTGAATAGCTGTTCTAATTATTATATATTCAGCTGATTAATAGGAG
TACTTGATAGGTGGACTGTGTCAGGTAGCCTCAGGCAATCCTACTTCAACAAGCTG
TCAGGGAGCCATGCCATGCTTCTTTATGACATAGGTGAATTTGATAGGCTCACTAG
CAGAACATGGGATCACAAGGTGGAACCNTTCCNTTT

Sequence ID 686

GACCCCTTCCTTACACCTTATACAAAAAAACTGAAACTGGACCCCTTCCTTACACC
TTATACAAAAATTAACTCAATTTTATTATGTTGTATTAAATTAAGTTGGGTTTAAT
TAAGATGGATTAAAGACTTAATTATAAGACCTAAAACCATAAAAACCCTAGAAGAA
AACCTAGGCCATACCATTCAGGACACGGGTATGGGCAAAGACTTCATAACTAAAAC
ACCAAAAGCAATGGCAACGAAGTCCAAATAGACAAATTGGACCTGATTAAACTAAA
GAGCTTCAGCACAGCAGAAGAGACTATCGTCAGAGTGAACAGGCAACCCACAGAAT
GGAAGAAAATTCTTGCAATCTATCCATCTGACAAGGGGCTAATATCCAAAATCTAC
AAAGAACTTAAACAAATTTACAAGGAAAAACACAAACAACCCCATCAAAAAGTGGG
CTAAGGATGTGAACAGACACTTCTCAAAAGAAAACATTTATGCAGCCAACAAACAT
GAAAAAAAGTTCATCATCACTGCTCATTAGAGACATGCAAATCAAAACCACAATGA
GATCCCATCCCACACCAGTTAGAATGGCAATCATTAAAAATGT

Sequence ID - 687 nt: 268

TTTATGTGTTTTTGCTTGGGGGGCGCTGGGCCTAGCCCAGAGTAGTGCTTGCTCCC
CCTGCCTTGTCCCACCAGGGAGGCAGCAGACTCAGGCCCTCCATGGTCCTCTTTGT
CATTTTGTTGACATGCATTCCTCCTTTTGTCATCTTGTTGGGGGGAGGGGATTAAC
CAAAGGCCACCCTGACTTTGTTTTTGTGGACACACAATAAAAGCCCCGTTTATTTG
TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID - 688 nt: 569

CTTTAGCCAGCCTGATCAGAAAAAAACAAAAGAAGAGGAAAGACGTAGATTACCAA
CATCAAGAATGTGAGTTATGATATCACTACAGACTCTCCAGGTATTAAAAGCATAA
TTAGAGAATGATATGAGCAGCTATATGCAAATAAGTTCAACATTGGACAAATGGAC
AAATTTCTTGAAAGATAAATTATGAAATTTCATTCTGAAAGAACTACATGACCTTA
ATTGTCTTACATCTATTAAATAAGTGGAAATTGTAGTTTAGAAACTTTCCCACAAA
GAAAACTCTAGGCCCAGATGGCATCAAAATAATATTCAGATGAATGAAATGGAGAA
AGGATAGCCTTTTCAACAAATGGTGGTGGAACAATTGGATTTCCATATGCAAAAAA
ATAGAGATGGACGCAGAGGTGTGTGCTTAGGAGGCTGAGGTGAGAGGATTGTTTGA
GGCCAGCCTGGGCAACATAGCAAGACCCCATTTCAAAAACAAAAATAAAGAACTTG
TAGCCTTACCTTGTGCCATATTATGAAAATGTATCATAGGCTTAAATGTGAAACGT
AAAACAAAA

Sequence ID 689

CGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAAGTTT
TTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAATAGG
TTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAAGATT

TTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAAAAGG
TTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTAT
TTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACTAATAGAAGG
GCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTTTAAA
AGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAACCGA
AGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGC

Sequence ID 690
CGAAAAGCAAATATAACTTGCCACTAACCAAGATCACCTCTGCAAAAAGAAATGAA
AACAACTTTTGGCAGGATTCTGTTTCATCTGACAGAATTCAGAAGCAGGAAAAAAA
GCCTTTTAAAAATACCGAGAACATTAAAAATTCGCATTTGAAGAAATCAGCATTTC
TAACTGAAGTGAGCCAAAAGGAAAATTATGCTGGGGCAAAGTTTAGTGATCCACCT
TCTCCTAGTGTTCTTCCAAAGCCTCCTAGTCACTGGATGGAAGCACTGTTGAAAA
TTCCAACCAAAACAGGGAGCTGATGGCAGTACACTTAAAAACGCTCCTCAAAGTTC
AAACTTAGATTTCAGATTT

Sequence ID 691
CCGGTCTCTACACAATATATAGAAATCTGGGCATGGTGGTGCCTGGCTGTAGTCTC
AGCTACCTAGTTGGGTGAGGTGGGAGAGTCGCTTGAGTCCTGGAGGTTGAGGCTGT
AGTGAGCCAGGGCTGCACCACTGCATTCCAGCCTGGGTAACAGAGTGAGACCCTGT
CTCAAAAAGAAAAAAAAAAATTGCTAATTTTAACAAATCACAAAACTGACTCAGGC
AAGTTGTCTGACTCAAAAGCCCTTGAAAAACCATCAAAGACAGTAGAATGTTAACT
GGTCATTTACGTAAAATAGTGTTCATTAAATTTTTGGTTCATTTAGGATAATCATT
TTAAATGAGACTGTATTTGAGACTGTATACACATACATATACATGTTTACACACAT
ATACGTACAATATATGTACATTCTATCTAAAAGATCATACATGTGTGTACATATAT
GTTTTTAAAAGTCAAACTGACATATTAATGGAAACAGTGCTTACATCTCTGGTAGT
GATTTTCTATTAGCAGCAGCCCTACATATGCTGCGTCTCTGAACAGCATGTCAGTG
CCATGACTGTCTAAACATGCAAATATGACTGACAGACTCTTGAGACAGCTTTCACC
TTG

Sequence ID 692
AATTCGNGGCCGCGTCNNCCTANGAGGCACCAGGAAATCCCGCGGGGTGGCCCATG
CAGACCAGGCGCACGTGGCTCATGGGGCANAATTGCCAAGGACAGCTCACGACAGT
GCCACCTTCTCACCATTCCAGCCAAGGAGAGATGTGACGTTGGAACTGCTCTGGCA
CTTCTGTCAAGCCTCCCCCGCCCCAATTGCCTTGAGATCTCTGCTCTTTGTCAGAG
ATTTGCAAAGACTCACGTTTTTGTTGTTTTCTCATCATTCCATTGTGATACTAAGA
AACTAAGAAGCTTAATGAAAAGAAATAAAATGCCTATGTTGTTGTTCT

Sequence ID 693

CTAGAACCCATGACTCCTAGGTCTTATACTGCAACCACAGTATCAGCAAATAATCT
TTCATAAGGGGATTATTCTCTGATTAACAGGAAATACAGGAATTTAATTTGTGAAC
ACGCTAGGTAGAAGCAGAAACCCAAATCCAAATCCAAATTTAAACATTTAAAATTC
ATTCTATAACTAAGATCTAACAGTCATTTTCTTCCCAGTAAGAAATAACCAAAGCA
TGCTAAAAATCACTGGACTAAATTGGTGTCAAAACTGCCACATTGCCAGGCATGGG
GGGGTCATACTTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGAAAATTGCTTGA
GGCCAGGAGTTCGAAACCAGCCTGGGCAACACAGTGAGACCCCATCTCCACAAAAA
AAAAAAATTAAAAAACAAAACAAAACATTAGCTGGGCATGGTGGTACACGCCTGTA
GTCCCAGCTACTCAGGAGCCTGAAGTGAGAGGATCACTGAAGCCCAGGAGGTAGAG
CTATGACTGTAGTGAGCTATGACTGTGCCACTACACTCCACCTGGGTGACAGGGGA
CTC

Sequence ID 694

CGACTTCCATTTGTATTAATGGAATACTAAGTCCCTCTGTGATTTCTGAACCAAGC
TATTCCTAGGCCTGAGTTTTATTTTGTTGACACAGAAATAAATTANAAGGCCAAGC
GTGGTGGCATGTGCCTGTAGTCCTAGTTGCTGAGGTAAGAGGATTGCTTGAGCCCA
GGAGTTCAAGGCTGCAGCAAGCTTTGATTGCGCCACTGCACTCCAGCCTTGGCGAC
AGACTAAGACGCTGTCTCAAAAAAAAACAAAAA

Sequence ID 696

GGTTATCAATGAGATTAAGAGACAACTAGAGTAAAAACAAAAGAAAAGAAAAGAAA
NGAAAACAACAGAAGCTCTATTAACTGACCTCTAACCAATACAACAGGTTAACTGA
TGTTCTCCATTCTGTATATAAAAATCCCAGTGGACACCCACAACACAGGCTTCAGG
CTTGTAGGACACTTTCTAGTTCATCTGAGCACTTTTGTTCTCAGCAGTTGAGCTGT
ATACTTAGCAACATTTGGTGCTTCCAAACCCATTTGTGCCTGTAGCACTTACTATT
GAAATACATAATTTAATTAAATATTATATAAAGGAATGGAATACGAGTTGGACAAG
AAAAAGAGTTAAATCTGAAGGTTAGGTAAAAAGAGCAACTTCTTTTCTCTGTTTTG
CAGGTTGGCAAAATCATTTAAAAACAATTGGAAGTATTATATGTTCTGCATTAAGT
TGTCATTTTACTTAAAAACTAGGCATCAAAGATGATGCATAATAAATTTAGTGTAT
GCAAGAATGACTGCTTGGGACCTCAATATATGAATTCTTAATCCAAGGAAAGTCCT
TGGCCTTACATTTAAAAGTCGGCAAATAAGTGTACGTTCATT

Sequence ID 697

GAACATTTAAAAATAATGCAAATAAGGCTGGGCGTGGGGGCTCACACCTGTAATCC
CAGCACTTTGGGAGGCCGAGGCAGGCAGATCACGAGGTCAGGAGATTGAGACCATC
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Sequence ID 698

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GGAGGGGCTGCTGAGTTCCCTTGTTCTAGCTAGCAGCACGCTCCTCANAGAGGGGG
CCGAGTTACAGACAGCAGCCGCATTCTCATGCAAAATTAGTTTAAACTGCTAGTG
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GCTCCGTAGAGACAGTTCAGCCAGTCATTTCTGCATTGGAGAGACTTCTCATACTT
TCTTTGAAGACTCATAGAAAGCTGGAT

Sequence ID 699

ATTAAGGTTTGTNCCCAACAAGAATAGATGTAATTAGAAAAAANTGNCTTCCTTAC
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ATAGTCAACCAGAAAAACTATCTGAATTAAAATAATTGGTCCATAGGTACTATTTT
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TGAGGAGCTTTGTANTCTAATAAAAGAGAAATATAAGTAAATGTTAGATATATGGG
NGGATAATGGTAACTATGTGCTTAAAGAGGTATAAAAGAAGGGTAGGGAGCAGATA
AGACAAAGGAAGGGCTATATTATAANGAAGAATATTCCAAGTAGGGAAGAGAAAAA
GATATGTTATCCATATAATATTTTATGTGCAGTAGAGAACATGTTCTATAGAANAG
ACAGAAGATG

Sequence ID 700

CTTGAGCCCAGGAATTCCAGCCTGGGCAATATAGTAAGACTCCGTCTCTACAAAAG
ATACAAAAATTAGCCAGATGTGGTGGTGCGTGCCTGTAGTTCCAGATACTGGAAAG
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TACGCCACTACACTCCAGCCTGGGCAACAGAGTAAGATCTTGTCTCAAAAAAAAAA
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CTTTGTTTTTCTCTCCTTGCCAGCTTCTCTGCAGCCTATAGCCTGCAGGCTGGCTG
CTGCGAGCCAGGACAAGCGGTGGGAAATGCAATCACAGCGTGAAATCTCTGTGTTC
AGAGACACGCAGGAAGCAGGTGAACCATGAAGGGCCAACACATGCCCCCAGTTAGC

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GTCCTGCCATTTGAAGCTGCAAGTGGCACACATGGATGCTGGACAGGCGCTCGCAC
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TGGGCCC

Sequence ID - 701 nt: 579
CTTTGGAGCTTCTGTCTGTGCTGTGGACCTCAATGCAGATGGCTTCTCAGATCTGC
TCGTGGGAGCACCCATGCAGAGCACCATCAGAGAGGAAGGAAGAGTGTTTGTGTAC
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TGACAAATATGCTGCAAGATTTGGGGAATCTATAGTTAATCTTGGCGACATTGACA
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AAAATACCTTATTTCAGTGATTCTAAGGCACCATTGATTAGAAACTGCATTATTAT
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Sequence ID 702
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TCGCTGCCGTCGGCAAAACGCATGGTTTTACGCGCTTCAACACCTTCCTGCACAAT
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TTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAAC
TTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAAGAGGC
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AAGCGTTAATATTTTGTTAAAATTCGCGT

Sequence ID 703
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ACCATGTCTGACAAACCCGATATGGCTGAGATCGAGAAATTCGATAAGTCGAAACT

GAAGAAGACAGAGACGCAAGAGAAAAATCCACTGCCTTCCAAAGAAACGATTGAAC
AGGAGAAGCAAGCAGGCGAATCGTAATGAGGCGTGCGCCGCCAATATGCACTGTAC
ATTCCACAAGCATTGCCTTCTTATTTACTTCTTTTAGCTGTTTAACTTTGTAAGA
TGCAAAGAGGTTGGATCAAGTTTAAATGACTGTGCTGCCCCTTTCACATCAAAGAA
CTACTGACAACGAAGGCCGCGCCTGCCTTTCCCATCTGTCTATCTATCTGGCTGGC
AGGGAAGGAAAGAACTTGCATGTTGGTGAAGGAAGAAGTGGGGTGGAAGAAGTGGG
GGTGGGACGACAGTGAAATCTAA

Sequence ID 704
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AAAATGCAAACAGAAACCACCACAGGAACAGCCCCTTGCTGCCTCCTGTTGCTGAG
GTAGTAGTCGCTAAAGAAAATTGAAGGCTCCTTACAATCTATATTTGAAAACTAGA
ACTTCTGTAGAAACACACAGATCCCGATCTTAGAAGTTGTACAGGACAATCTGGTA
AAACTGACATAATTGTGATTTATTAACATGAATTAAAATGCCCAACCAGTGCTTCA
GTGTGACAGTATATTTAAAATAAAAAAGAAATTAAAGGTCATATACTGTACTACTT
TCACAAAGATCCACAGTTTTGCAAAAGACTTGTCATATGTACAATGCTATATATCA
AATGAGAAAAGCTGTAAGCAATTATATACGCAAAAGAAATGGCAGTA

Sequence ID 705
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ATACGCAGACATTGTGGCATCTGGGTAGAAGAATACTGTATTGTGTGTGCAGTGCA
CAGTGTGTGGTGTGTGCACACTCATTCCTTCTGCTCTTGGGCACAGGCAGTGGGTG
TAGAGGTAACCAGTAGCTTTGAGAAGCTACATGTAGCTCACCAGTGGTTTTCTCTA
AGGAATCACAAAGGTAAACTACCCAACCACATGCCACGTAATATTTCAGCCATTCA
GAGGAAACTGTTTTCTCTTTATTTGCTTATATGTTAATATGGTTTTTAAATTGGTA
ACTTTTATATAGTATGGTAACAGTATGTTAATACACACATACATATGCACACATGC
TTTGGGTCCTTCCATAATACTTTTATATTTGTAAATCAATGTTTTTGGAGCAATCC
CAAGTTTAAGGGAAATATTTTTGTAAA

Sequence ID - 706 nt: 496
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GCGTGCCCCTCTGGAGAAGGCCCTGGATGTGATGGTGTCCACCTTCCACAAGTACTC
GGGCAAAGAGGGTGACAAGTTCAAGCTCAACAAGTCAGAACTAAAGGAGCTGCTGA
CCCGGGAGCTGCCCAGCTTCTTGGGGAAAAGGACAGATGAAGCTGCTTTCCAGAAG
CTGATGAGCAACTTGGACAGCAACAGGGACAACGAGGTGGACTTCCAAGAGTACTG

TGTCTTCCTGTCCTGCATCGCCATGATGTGTAACGAATTCTTTGAAGGCTTCCCAG
ATAAGCAGCCCAGGAAGAAATGAAAACTCCTCTGATGTGGTTGGGGGGTCTGCCAG
CTGGGGCCCTCCCTGTCGCCAGTGGGCACTTTTTTTTTCCACCCTGGCTCCTTCA
ACACGTGCTTGATGCTGAGCAAAGTTCAATAAAGATTTTGGGAAGTTT

Sequence ID - 707 nt: 397
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ATGGCTTGAACCCAGGAGGTGGAGCTGACAGTGAGCCGAGATCGCGCCACTGCACT
CCAGCCTGGGCGGCAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAATAGA
CTTTGAGACCAGCCTGACCAACATAGTGAAACCCGTCACTACTAAAAATACAAAAA
TTACCCGGGCGTGGTGACGGGCGCCTGTAATCCCAGCTACTTGGGAGGCTGAGACA
GGAGAATCACTTGAACCAGGGAGGCGGAGGTTGTAGTGAACTGAAATCGTGCCCCT
GCACTCCAGCCTGGGTAACAAGAGCGAAACTCCGTCTCAAAAATAAATAAATAAAT
AAAAT

Sequence ID - 708 nt: 293
CCAGCTTTTTATGGTGTTTAATCTAATACACTTAAGCTGCAGTCCCAAAATTAGGG
GTCCTTCAGTCTTGGAGACTATAAGGGAGCCTCTGCACCCAGGGAAAATGTTACCC
TTTACAGGGGGGAAGGGTAAACCAGTAGGGAATACAGTACAATCCCAACCCTACTG
GGAGGGGCGGGAGGGAGGTGTTGCCGTCACTGTATTAAGTCGATGTTGGGAAACGT
TTTAACATCTGGAGCCTTTGTGGGTGGAAATATGTCTCCAGTTACAACTCCGCAGT
GGATGTGAAGAAG

Sequence ID 709
GGAAGCTACAATGATTTTGGGAATTACAACAATCAGTCTTCAAATTTTGGACCCAT
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ACTTTGCAAAACCACGAAACCAAGGTGGCTATGGCGGTTCCAGCAGCAGCAGTAGC
TATGGCAGTGGCAGAAGATTTTAATTAGGAAACAAAGCTTANCAGGAGAGGAGAGC
CAGAGAAGTGACAGGGAAGCTACAGGTTACAACAGATTTGTGAACTCAGCCAAGCA
CAGTGGTGGCAGGGCCTAGCTGCTACAAAGAAGACATGTTTTAGACAAATACTCAT
GTGTATGGGCAAAAAACTCGAGGACTGTATTTGTGACTAATTGTATAACAGGTTAT
TTTAGTTTCTGTTCTGTGGAAAGTGTAAAGCATTCCAACAAAGGGGTTTTAATGTA
NATT

Sequence ID 710
TGGATTCCCGTCGTAACTTAAAGGGAAACTTTCACAATGTCCGGAGCCCTTGATGT
CCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAG

GTGGCACCAATCTTGACTTCCAGATGGAACAGTACATCTATAAAAGGAAAAGTGAT
GGCATCTATATCATAAATCTCAAGAGGACCTGGGAGAAGCTTCTGCTGGCAGCTCG
TGCAATTGTTGCCATTGAAAACCCTGCTGATGTCAGTGTTATATCCTCCAGGAATA
CTGGCCAGAGGGCTGTGCTGAAGTTTGCTGCTGCCACTGGAGCCACTCCAATTGCT
GGCCGCTTCACTCCTGGAACCTTCACTAACCAGATCCAGGCAGCCTTCCGGGAGCC
ACGGCTTCTTGTGGTTACTGACCCCAGGGCTGACCACCAGCCTCTCACGGAGGCAT
CTTATGTTAACCTACCTACCATTGCCCTGTGT

Sequence ID - 711 nt: 498
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AGGTGGAATTTACAGAAGCAGAGAGTAGAATGGTGATTACCAGAGGCTGGGGAGTG
AGGGCAGGAGGTTGGAGAAATGTTGGTCAAAGGATACAAAGTTTCAGTTATACAGG
ATGAATAAGTTCAAGAGATCTATTGTACAACGTGGTGGCTATAGTTGATAACAATG
TATTGTGTTCTTGAAAAATGCTGAGAGAGTAGATTTTAAGTGTTCTCACCACAAAA
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GTATTATACATATTTCAAAACCACGTTGTACATGAGAAAGATACACAATT

Sequence ID 713
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TTTGGAAATCCTGGCTGCCATTTTTGCAGCTGCCATCCATGACGTTGATCATCCTG
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GATGAATCTGTGTTGGAAAATCATCACCTTGCTGTGGGTTTCAAACTGCTGCAAGA
AGAACACTGTGACATCTTCATGAATCTCACCAAGAAGCAGCGTCAGACACTCAGGA
AGATGGTTATTGACATGGTGTTAGCAACTGATATGTCTAAACATATGAGCCTGCTG
GCAGACCTGAAGACAATGGTAGAAACGAAGAAAGTTACAAGTTCAGGCGTTCTTCT
CCTAGACAACTATACCCGATCGCATTCAGGTCCTTCGCAACATGGTCACTGTGCAG
ACCTGAGCAACCCCACCAAGTCCTTG

Sequence ID 714
CTGTAACAGAGATTCCTTTTTTCAATAATCTTAATTCAAAAGCATTATTAGACTTG
AAAGGGTTTGATAATCTCCCAGTCCTTAGTAAAGATTGAGAGAGGCTGGAGCAGTT
TTCAGTTTTAAATGAGTCTGCAGTTAATATCAAATGTGAGTTTGGGACTGCCTGGC
AACATTTATATTTCTTATTCAGAACCCTTGATGAGACTATTTTTAAACATACTAGT
CTGCTGATAGAAAGCACTATACATCCTATTGTTTCTTTCTTTCCAAAATCAGCCTT
CTGTCTGTAACAAAAATGTACTTTATAGAGATGGAGGAAAAGGTCTAATACTACAT

AGCCTTAAGTGTTTCTGTCATTGTTCAAGTGTATTTTCTGTAACAGAAACATATTT
GGAATGTTTTTCTTTTCCCCTTATAAATTGTAATTCCTGAAATACTGCTGCTTTAA
AAAGTCCCACTGTCAGATTATATTATCTAACAATTGAATATTGNAAATATACTTGG
CTTACCTCTCAATAAAAGGGTCTTTTCTATT

Sequence ID 717
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AGCCCGATACTAGGACTTATGCAGAAAAAACCTTGACATGGAGGAAAGTAAGATCT
AAATAAATACTGTATTCATAGATTAAAAGACTCAGCATAATAAATATACCATTTCT
CCCCAGATTGATGTACAGATTTAACACAATTCCTATCAAGATCCCAGCAAGATTTT
TGTAGATATGTAAAAGATTATTCAAAAATGTAAAAGGAAGGACAAAGGACTAGAAT
AGATAAAACAAAATGGAGAAAGATTTAATAGGAATCACTGTAACTGATTTTAAGAC
ATACAGAACAATAATAGAAACTGCTTGTATTAGTCCATTTTCACGCTGCTGATAAA
GACATACCTGAGATTGGCAATTACAAAGGAAAGANGTTTATTGGCTTACAGTTCCC
ATGGCTGGGGAGGCCT

Sequence ID 718
CTCCTCTGGGTTGAAACCCGGGCGCCGCCAAGATGCCGGCTTACCACTCTTCTCTC
ATGGATCCTGATACCAAACTCATCGGAAACATGGCACTGTTGCCTATCAGAAGTCA
ATTCAAAGGACCTGCCCCCAGAGAGACAAAAGATACAGATATTGTGGATGAAGCCA
TCTATTACTTCAAGGCCAATGTCTTCTTCAAAAACTATGAAATTAAGAATGAAGCT
GATAGGACCTTGATATATATAACTCTCTACATTTCTGAATGTCTGAAGAAACTGCA
AAAGTGCAATTCCAAAAGCCAAGGTGAGAAAGAAATGTATACGCTGGGAATCACTA
ATTTTCCCATTCCTGGAGAGCCTGGTTTTCCACTTAACGCAATTTATGCCAAACCT
GCAAACAAACAGGAAGATGAAGTGATGAGAGCCTATTTACAACAGCTAAGGCAAGA
GACTGGACTGAGACTTTGTGAGAAAAGTTTTCGACCCTCAGAATGATAAACCCAGC
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Sequence ID 719
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GGCTGGCAAATGGCCATTTCCCTTCCACTTGAATAGAGACCCATAACTCAAGTATC
TGCCCTTAAGACACCACAGGACTGTTCTTCGCGGGCCCTGCCCCTGGATTTGGGAG
AGGCAGTCCANCTCACCCAACTAGGCTCTGCANGGGGACCANGAGGGATGGGTTGT
GTCCACAGGACCAGCCAGACTGATGAGGGATGCGGCAAGCATATTCTCACCACCTT

CTTTCACGTTTACAACANACCAGCNTTCCCTGTGTGGCAGGGGTTACATTGGTCAC
CGAGGACCTANAATCATGGAGTGCTCTGGGGATCCGGGCTTGGA

Sequence ID 720
TCAGTGTTGAATTTTGTCAGACACTTTCTCTGCATCAATTGGTATGACCATGTGAT
TTTTTTTCTGTAGCCTGTTAATATGGTTAATTTTCAAATATTGAGCTGATTAATTT
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GTGTCTGTTTTCATGATAGATACTGGTCTATAGTTTTGTTGTAATATCTTGGTTTG
ATTTTGATATCAGGATAATGCTACCTTAATAGAATGAATTGGAGCCAAGTATGGTG
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Sequence ID 721
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TGGCGAGGTACTAACTGAGAAACTTTTTCATGCTTTATGCCTACCTCTTGTAGTTG
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GCTCCTCCCCCAGCCCACCCCGTCTTCCCTTAACATTTTTTCAGGGGGGGTTGGGA
GTGGTTTCATTTTAATGTGAGTGGATGTTTTGATAGTTGTAAGGAAAAAATGCATT
TCAGACACATTTCACACATGAGCTATTTTCTTACACAGTATGTCTTATTGGTAATA
AGAATGTAATTCAT

Sequence ID 722
CNTTCCNTAAGAATACAAAAAATTAGCTGGGCGTGGTGGCAGGCGCCTGTAATCCC
ATCTACTCAGGAAGCTGAGGCTGGAGAATCGCTTGAACCCGGGAGGCGGAGGTTGC
AGTGAGCAGAGATCACGCCACTGCAGTCCAGCCTGGGCAACAGTGCGAGACTCTGT
CTCAAAAAAAAAATAAATAAATTACCTGGGTGTGGCAGCGCGTGCCTGTAATCCCA
GCTACCCAGGAGGCTGAGGCAAGAGAACTGCTTGAACCCAGGAGGCAGAGGTTGCA
TGGAGCTGAGATGGCGCCACTGCACTCCAGTCTGGTGACAGAGTGAG

Sequence ID 724
CTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGNGGTGCATGCCTGTAAACCC
AGCTACCAGGTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCAGGGAGTCGG

AGGTTGCGGCGAGCTGAGATCATGCCACTGCACTGCGGCCTGGAGACAAGAGCAAG
ACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGACNTCACCTAATTGCAG
NGNGNGGACCTTATTTGGCTNTTAATTCAAACTATTAAAAATGTGAACN

Sequence ID - 726 nt: 260
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GGGCTCTGCCCTCCCTCCTTCCTTCTTGCTTCTCATAGCCCCGGTGTGCGGTGCAT
ACACCCCCACCTCCTGCAATAAAATAGTAGCATCGG

Sequence ID 727
CTGAGTNTAGAAATGATGCCATTAATACTGATTGCAAAAACATTACAACTCAGTAC
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TCTCAGGAAACTGTATATACTCTGTACTTTTATGCAACTTTATCAGATCATTTCAG
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TATGTACCTTTTGTTTATTTTGCTGTCAACATCTAAATAAAGGTTTTTTTGTTTGT
TTTTTGTTTTTTTAATTGTTTTGTTTTAAAGATTGTTTTAATTAATTAAAAAATTA
ATTGTTTTAATTAAACAATTGTTTAATTGTTTTAAAGTCGCCAGGCTGAGGCAGGT
GAATCACAAGCTTAGGAGTTGGAGGCTAGCCTGCCAACATGGTGAAACCCCGTCTC
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Sequence ID 728
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TAAAAAAGATTCAAGAGCAGTGAGGTTTGTTCTTTCCAGTGAATGGTGGACTGAGT
GGTGCGAGGTGGAGGGCTAACAAGAGGAAAGAACTACATTCTTCAGAATACAGTGA
TGAAAATTCATTTTGAAACTCAAATATTTTCATTTTGGATATTCTCCTGTTTTTAT
TAAACCAGTGATTACACCTGGCCATCCCTCTAAATGTTCTAGGAAGGCATGTCTAT
TGTGATTTTGATGAAGACAGAATTATTTTTCTCTGTAGAAACACAGATACCACTTT
ATCAGGGGAAGTTAGTCAAATGAAATGGAAATTGGTAAATGGACAAAAGCTAGCTA
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CATAGTTTAACATCTTGAGAAATTTGGGACATAAAAGTTTTCATNGGTAGACAGTT
CATGGCAGTATATGAATTGACATAATGGAAATAATCTGATTTTATTTTTACAACTA
ACATCCTTTCCCC

Sequence ID - 736 nt: 641

GGAATTCCAAGTGCTTGGGGATAATGATACCTCTGACCTTTCTTCCTTTTGGGAAG
TACTTGAGTGTGCAGCTGCATGAGGCCTCAGCAGGAGAGAGATTTTAGGTCCAAGA
AGCTATACCAGTAGGACAAGGCAGGAAAATACTACACTTTCAGGATCAAGCCCCTC
TGACTCTCATTTGGAAACTGGATGTTTGCTAAGCACCTGCTTCTTAAGGATGCCGA
GGGATTTAATGATACTCCCAGAAACCTGGAGAGATTAATGGGGCCTATGGAGAAGT
GCTCTGAACTCAGTGTTGGGACTTGAATAAAATTAACCATTGTCATGTTTTCAGAA
CAACTAAGCTGTTTTATATTTCATGTGCATGAAAGCCCTAGAACTAAGTTGTGTTA
TTTCCAGAAATGAAATAGATCCCACAGTTAGATGATGTGGCCATTAGGAAGTACCA
AATTTATAAAAATCACTGGAGGTCTGTCTGAGCAGTACCTAATAAAATATAGTATA
CTGAAAGTGAACAGATACTTTGTCTCTTTCTTTGGCTGCTTGATCTTTATCTGTGT
CTGCCGTACAGTGCACCCTTAAAGTATTCTACACCAGTGCTTCTCAAACTGGAAAT
GTGCATGTAAGTCACCCANGGGTCT

Sequence ID 739

TGCATGCCCATAGTCCCAGCTATTTGGGAGGCTGAGGCAGGAAAATCGCTTGAACC
CGGGAGCCAGAGGTTGCAGTGAGCCGAGATCGCACTCCAGCTTGGCGACAGAACAA
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TGCTGTTTGTAGATGTTAATTAATCAAACCTTTCTCTACTCATTCTGGACCAGTTA
AGGTTTTCTCCTTCTCCGTATGAGTTTTGATTTTCGTCCTCCTTGGTTGGAGATCA
CACTTTGGTCTGCTGCTAAGTTGGATGCCTCCCACTGTCTTTCCCTAAGTCTAGGG
CTTCANACCCCAGTGTGGGGAGAGGGACTTTCGTTTCCTGCCCCTCACCACATCAG
ACACAGGCAGGCAAGAATAAGATGGCCAAAAGGCCGATGAACTTCTTGACCTAGCC
TGGGACATTACCTGTTACTAGGTGGACTTCACTGCCTGTGAATGGAAGCTGAAGGG
CTGTTTTTTTGGTTTGTATTTGGACAGGCCAGGCTTANAGAGGGAGAGAACTGGGC
TACTCTTCAGCAGTGATCTTTAAAATGCC

Sequence ID 747

CAGAGTGCAAGACGATGACTTGCAAAATGTCGCAGCTGGAACGCAACATAGAGACC
ATCATCAACACCTTCCACCAATACTCTGTGAAGCTGGGGCACCCAGACACCCTGAA
CCAGGGGGAATTCAAAGAGCTGGTGCGAAAAGATCTGCAAAATTTTCTCAAGAAGG
AGAATAAGAATGAAAAGGTCATAGAACACATCATGGAGGACCTGGACACAAATGCA
GACAAGCAGCTGAGCTTCGAGGAGTTCATCATGCTGATGGCGAGGCTAACCTGGGC
CTCCCACGAGAAGATGCACGAGGGTGACGAGGGCCCTGGCCACCACCATAAGCCAG
GCCTCGGGGAGGGCACCCCCTAAGACCACAGTGGCCAAGATCACAGTGGCCACGGC

CACGGCCACAGTCATGGTGGCCACGGCCACAGCCACTAATCAGGAGGCCAGGCCAC
CCTGCCTCTACCCAACCAGGGCCCCGGGGCCTGTTATGTCAAACTGTCTTGGCTGT
GGGGCTAGGGGCTGGGGCCAAATAAAGTCTCTTTCCTC

Sequence ID - 757 nt: 583
GAACCCTGCGGAGGGACTTCAATCACATCAATGTAGAACTCAGCCTTCTTGGAAAG
AAAAAAAAGAGGCTCCGGGTTGACAAATGGTGGGGTAACAGAAAGGAACTGGCTAC
CGTTCGGACTATTTGTAGTCATGTACAGAACATGATCAAGGGTGTTACACTGGGCT
TCCGTTACAAGATGAGGTCTGTGTATGCTCACTTCCCCATCAACGTTGTTATCCAG
GAGAATGGGTCTCTTGTTGAAATCCGAAATTTCTTGGGTGAAAAATACATCCGCAG
GGTTCGGATGAGACCAGGTGTTGCTTGTTCAGTATCTCAAGCCCAGAAAGATGAAT
TAATCCTTGAAGGAAATGACATTGAGCTTGTTTCAAATTCAGCGGCTTTGATTCAG
CAAGCCACAACAGTTAAAAACAAGGATATCAGGAAATTTTTGGATGGTATCTATGT
CTCTGAAAAAGGAACTGTTCAGCAGGCTGATGAATAAGATCTAAGAGTTACCTGGC
TACAGAAAGAAGATGCCAGATGACACTTAAGACCTACTTGTGATATTTAAATGATG
CAATAAAAGACCTATTGATTTGG

Sequence ID - 758 nt: 424
CTTGGCTCCTGTGGAGGCCTGCTGGGAACGGGACTTCTAAAAGGAACTATGTCTGG
AAGGCTGTGGTCCAAGGCCATTTTTGCTGGCTATAAGCGGGGTCTCCGGAACCAAA
GGGAGCACACAGCTCTTCTTAAAATTGAAGGTGTTTACGCCCGAGATGAAACAGAA
TTCTATTTGGGCAAGAGATGCGCTTATGTATATAAAGCAAAGAACAACACAGTCAC
TCCTGGCGGCAAACCAAACAAAACCAGAGTCATCTGGGGAAAAGTAACTCGGGCCC
ATGGAAACAGTGGCATGGTTCGTGCCAAATTCCGAAGCAATCTTCCTGCTAAGGCC
ATTGGACACAGAATCCGAGTGATGCTGTACCCCTCAAGGATTTAAACTAACGAAAA
ATCAATAAATAAATGTGGATTTGTGCTCTTGT

Sequence ID - 764 nt: 626
GATTTTTTTTTTTTTTTTGAGATGGAGTCTTTCTCTGTCGCCCAGGCTGGAGTGCA
GTGGTGAAATCTCGACTCACTGCAACCTCCGTCTCCTGGGTTCAAGCAATTCTCCT
GCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCAGCCACCACGCCCGGCTAAT
TTTTGTATTTTTAGTAGAGACAGGTTTTCACCATGTTGGCTAGGCTGATTTTGAAC
TCATGACCCCAAGTGATCTGCCCGCCTCGGCCTCCCAAAGTGCTGGAATTACAGGT
GTGAGCTACCACTCCCAGCCAATGATTACATTTATAAGGTAAAATAACTTGTGCCA
ATCTGTACAAGTGAATTCAGATTTAAAATTTTAATTGTAAAAAGATATCCAGGTGA
TATTTCTCCCTGAATAATTTAGTTTCCTTTTCTATTTCTTGATATAAAAGTACTCA
GCATTGAAGTAATTGCTATCTTCACATTTCTTCCTATTTGAGCTGTCTAAATAAGT

AGTCCTACATATTTTCCCCCCAACACAAAAAACCCAGAAAAGAATTATTTTATACT
GGATTTTTTTGGTTGTAGCAGGAACCTAAAGGNGCCAATTGTAACATGCATGTTCT
TTTTGGCAAA

Sequence ID 766

GTCCATCCTGCAGGCCACAAGCTCTGGATGAGGAACTTGAGGCAAGTCACCAGCCC
CTGATCATTTCGCCTAAAAGAGCAAGGACTAGAGTTCCTGACCTCCAGGCCAGTCC
CTGATCCCTGACCTAATGTTATCGCGGAATGATGATATATGTATCTACGGGGGCCT
GGGGCTGGGCGGGCTCCTGCTTCTGGCAGTGGTCCTTCTGTCCGCCTGCCTGTGTT
GGCTGCATCGAAGAGTAAAGAGGCTGGAGAGGAGCTGGGCCCAGGGCTCCTCAGAG
CAGGAACTCCACTATGCATCTCTGCAGAGGCTGCCAGTGCCCAGCAGTGAGGGACC
TGACCTCAGGGGCAGAGACAAGAGAGGCACCAAGGAGGATCCAAGAGCTGACTATG
CCTGCATTGCTGAGAACAAACCCACCTGAGCACCCCAGACACCTTCCTCAACCCAG
GCGGGTGGACAGGGTCCCCCTGTGGTCCAGCCAGTAAAAACCATGGTCCCCCCACT
TCTGTGTCTCAGTCCTCTCAGTCATCTCGAGCCTCCGTTCAAAATGATCATCATCA
AAACTTATGTGGCTTTTTGACCTTTGAATAGGGAATTTTTAAAATTTTTTAAAAA
TT

Sequence ID 768

CCAGCGCAGGGGCTTCTGCTGAGGGGGCAGGCGGAGCTTGAGGAAACCGCAGATAA
GTTTTTTTCTCTTTGAAAGATAGAGATTAATACAACTACTTAAAAAATATAGTCAA
TAGGTTACTAAGATATTGCTTAGCGTTAAGTTTTTAACGTAATTTTAATAGCTTAA
GATTTTAAGAGAAAATATGAAGACTTAGAAGAGTAGCATGAGGAAGGAAAAGATAA
AAGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAAT
GTATTTAAAAGAAAATTGAGAGAAAGGACTACAGAGCCCCGAATTAATACCAATAG
AAGGGCAATGCTTTTAGATTAAAATGAAGGTGACTTAAACAGCTTAAAGTTTAGTT
TAAAAGTTGTAGGTGATTAAAATAATTTGAAGGCGATCTTTTAAAAAGAGATTAAA
CCGAAGGTGATTAAAAGACCTTGAAATCCATGACGCAGGGAGAATTGCGTCATTTA
AAGCCTAGTTAACGCATTTACTAAACGCAGACGAAAATGGAAAGATTAATTGGGAG
TGGTAGGATGAAACAATTTGGAGAAGATAGAAGTTT

Sequence ID 773

GAGGAAAGGGGAGTTAATATTTAGTGGACAGAATTTCAGTTTTACAGATGAAAAGA
GTTCTGGAGATAGACGGTGTTGATAGTTGCACAGCAGTGTGAATGTGCTCATTGTT
ACCGAACTTAAAAATGTTTAACATAGTATTATGTGATTTTTATTTTGCCACTTAAA
AAAAAAGAATGAAGTACTGATACATGCTACAACATGGGTGAGCTTTAAATACATTC
TGCTCAGTGAAATAAGCCAGATGCAAAAGATCACATATTATATAATCCACTTATAC

GAGATACCTAGAATAGGCAAATTCATAGAGACAGAAAGTAGAATAGTGGTTCCCAG
GGGCTGGGGACAAGGGGGCAGTGAGAGATTGAGAGTTATTATTAATGCGTACAGAG
TTTCAGTTTGGGCTGATAAAAAAGTTCTGAAGATGGATGGTGATGATGGTTGTACA
TCAATGTGAGTGTAATTACCGCCACTGAACTGCCCTTAAAAACGTTTAAAAGAGTA
AATTTTATGTTGNGTATATTTTACCATAAT

Sequence ID 776

TTTTTTTTTCATAAGAGGCAAGTACAAGAAAAAGCTTAATTACTTTAACTTCTAAG
TAGTTTGGAATCTAAATAAATAGGAGTTACCAAATATATGCGCTTCTGTGAATAGT
TTTCCCCCACATGTTTATTTATATTTTTGCATCTCATCAAACCTAACAGATTCTAA
AGTCTCTGGTGATAATGACAATATCTGCTACGGAGAGACTAGCCTGGGGGAAGAGG
ATCTCCCTGAACAAGGATAGCGGAGTTGCTGCAGCTTTCAAATGAAGCTGGACATT
TAGCTGCGGGGGTAGCACCCTTTGATCAAGGCAGCCCAAAGATGAGTTTCAGGGAT
GGGACTGACAGAAGAGAAAAGTTCTTCCCAGCCCTTTCTACTTTTTCTCTTTGTTT
CTCAGGCTTCTGGCCGTCTTCAGTTTTCACAAGTTTCACTCTCAACCCTAAACAGT
ACTTCTGTGAAGTACCCTTTGGCCCCTCGTTTTCAGCTCCTAAACTCACCTGGAAA
TAGATGTCAATCTAATTTTGGGTCTGACTAGTGCAGTAGGCATTTTTGGTGA

Sequence ID 782

CTCACACAGAACAAAAATGAATGAGTGTGGCTGTGTGCCACTATCACTGTGTCTAC
AAAAACAGCCAGTGGGCCTGATTTGGCCCTTGGCTGCAGTGCGCCCGTCTCTGTTT
TTGAGGAATAAAATCGCATCATTTCATATGGCTAATGCAATTTTTTTCCCATCTGG
AAGCAACATCTGATTGGACTCATCTTGTATGGTGCTTGTTACAGTCTCTGTAAATG
GGAGAGGGTCCGAGAATAGCTCTTCCTGTTTTCATCAGGACTGTTTTTAGGGATGG
CAAAGAAGTCAGTGTGTCCAGCCTGTGTCCTCCTCACCACGTGGCTGATTCCTGAA
TCTGCATGTGCANCACNTGCCGTTGTCTGGGGCATGATCTGTGTGA

Sequence ID - 785 nt: 556

CTTTTCTCTGGGTATAGATTTACCCTAGCACCTATCTCATTATATTGAATTTTCCA
GCATATTTAAATAAACTATTAATTAGTCACACTATTTCTTAAAAGTCACACTATCA
ACTAATCGTGACCGCAATTATCTAGGGGTGATAATCTGCTGAGTCTACTCTTTAAA
TACACTGGGACCCAGCATATTGAGTTATATTGGCACAGAAACTTCACTCTGGGTAT
AGATTTACCCTAGTACCTTGCCGGCAGGATCCTATTATTCATGGTTGTACAAGCAA
GGTTCAGGGAAGAGGCTGGCACAGAGAAGGTACCTGGTAACTGTTGTTTGAGGCTG
AATTCAGCTCAACTCAGCTCCAGTAGAGATGGTGTCCCCTTCTCTACCGTGTTGAG
ATAGTGTGCAGTCCCTTCCTAAGGGCTGTTACCCACCGCAATAGGACTTGTCAGCT
TCAACTTTTAAATTTCTCTGCTCCCGCTGGGACCCACCCGCTTCAAAAATCATCAT

GGNGGNTTTAGCACCAATTTAGTAAACACAAACTGTCTGAAATATTTTGGAT

Sequence ID 796

GAACATTCAAGATAGTGAGAGGAAGAAAAAGATATGGCTGTACGGGACCGAGGTCT
CTTCTATTATCGCCTCCTCTTAGTTGGCATTGATGAAGTTAAGCGGATTCTGTGTA
GCCCTAAATCTGACCCTACTCTTGGACTTTTGGAGGATCCGGCAGAAAGACCTGTG
AATAGCTGGGCCTCAGACTTCAACACACTGGTGCCAGTGTATGGCAAAGCCCACTG
GGCAACTATCTCTAAATGCCAGGGGGCAGAGCGTTGTGACCCAGAGCTTCCTAAAA
CTTCATCCTTTGCCGCATCAGGACCCTTGATTCCTGAAGAGAACAAGGAGAGGGTA
CAAGAACTCCCTGATTCTGGAGCCCTCATGCTAGTCCCCAATCGCCAGCTTACTGC
TGATTATTTTGAGAAAACTTGGCTTAGCCTTAAAGTTGCTCATCAGCAAGTGTTGC
CTTGGCGGGGAGAATTCCATCCTGACACCCTCCAGATGGCTCTTCAAGTAGTGAAC
ATCCAGACCATCGCAATGAGTAGGGCTGGGTCTCGGCCATGGAAAGCATACCTCAG
TGCTCANGATGATACTGGCTGTCTGTTCTTAACAGAACTGCTATTGGAGCCTGGAA
ACTCAGAATGCAGATCTTTTGTGAACAAAATGAAGCAAGAACCGGAGACNCTGAAT
AGTTTTATTTCTGTATTAAAAACTGNGATTGGAACAATTGAAGA

Sequence ID 801

CCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAAAGTAT
AGGCGATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATGA
AAAATTATAACCAAGCATAATATAGCAAGGACTAACCCCTATACCTTCTGCATAAT
GAATTAACTAGAAATGAGGATTCTGACCTTGACTTTGATATCAGCAAATTGGAACA
GCAGAGCAAGGTGCAAAACACAGGACATGGAAAACCAAGAGAAAAGTCCATAATAG
ACGAGAAATTCTTCCAACTCTCTGAAATGGAGGCTTATTTAGAAAACAGAGAAAAA
GAAGAGGAACGAAAAGATGATAATGATGATGAGTCAGGTAAAAGTTCCAGAAATGT
GAACAACAAAGATTTTTTTGATCCAGTTGAAAGTGATGAAGACATAGCAAGTGATC
ATGATGATGAGCTGGGTTCAAACAAGATGATGAAATTGCTGAAGAAGAAGCAGAAG
AAGGAAGCATTTCTGAAATATGAATGAAAAAAATTACATCTTTAGAAAAAGAGTTA
TTAGAAAAAAGCCTTGGCAGCCGTCNGGGGGAAGTGACGCACAGAAGAGACCAGAG
AATAGCTTCCTGGANGAGACCCTGCACTTTACCCATGCTGCTGGATGG

Sequence ID - 808 nt: 641

CCGGGTTTTAGTATTTAACCAAGAGCCTTTTAAATATTGAAAACCCATAGTTCAGA
AAATGTTAGTATTGCTGCCCTTCTTCACATAAATTTTTTTTTAAATTATACTATTA
TTTTGCTTAATTTTATATTGGGTTAAAACAACCTTCAAGAAGGTTAACTAGGAAAG
AAGACCTTTTTGTTTTATTTTTACTATTTATATATAGAAGACAAATCAGCATTTGG
TGATAGTTTTACATGACCAGTTATCAAACGGTCATAGTATGAAGTGTGCAGTTGTT

CATTATTAGTAAATTATGTTTGATTTTTAAACTATTTAGTACTAATAGTTGAGATG
AAAACTGAAGAAAAATGCCAATGTGACGTTTGTGTATAGCTAGCCTTAAAAAACTT
CCCATGTTTTTAGGTGACTTTTTTCCCCCTCTTAGTACTCTGGAGAAACAATGAAG
ATGGGCCATCTCAATTCCAGATGTAAACAAAAAGTAATTTTTATTTCAACATTTAA
TGTAACTGCTATTATTGNGGATTCTTGNCTTGNGTATTTTCTTTCCCTTATTCAAG
TAATATAGAATAACTTTCCTTAAAATGATTTGATCCAAGATACGTCATTTCTGTAT
TGGCAAAATGCCNCTATTAAAGTGT

Sequence ID - 814 nt: 132
GTTAAAGTGATACATTTTTATACCAAATGTGTTTATTTTTTTGTGCAAGTAATCCT
TAAAATTGCAATTGTATTAGGTGTTAAAATAAAGTTTTTAAAAAATTAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

Sequence ID 817
GACAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAAC
CTGGCGCAATAGATATAGTACCGTAAGGGAAAGATGAAAAATTATAACCAAGCATA
ATATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACT
TTGCAAGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAG
CTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGAAGATTTATAGGTAGAGG
CGACAAACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCA
ACTTTAAATTTGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTC
CAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAA
TTTAACACCCATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTC
AACACCCACTACCTAAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATT
GGACCAATCTATCACCCTATAGAAGACTAATGTTAGTATAAGTAACATGAAAACAT
TCTTCTNCGCATAAGCCTGCGTCAGATTAAAACACTGAACTGACAATTAA

Sequence ID - 821 nt: 370
AAAGAGCTCCCAAATGCTATATCTATTCAGGGGCTCTCAAGAACAATGGAATATCA
TCCTGATTTANAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCTC
AAAGCAATACCAGGATAGCTGTTGTTTCANAGAAAGGATCGTGTGCTGCATCTCCT
CCTTGGCGCCTCATTGCTGTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGAT
AGCTGTGGTCCTGGGTACCATGGCTGGTTTCAAAGCTGTGGAATTCAAAGGATAAA
TTAATGAAGAAAACAAGCGGAGCTGAAGAAGAAAGTACAATATGGTGCTGTCTTCC
TAATGAAATAAATTCACTAAATGGACATTAAAAA

Sequence ID 825

AGACTCGAGCAAGCTTATGCATGCATGCGGCCGCAATTCGAGCTCGGCCACTTGGC
CAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTC
GTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT
TTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTT
GCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGC
GTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAA
TCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGG
AACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGT
CTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGT
CGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAAAGCT
TGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAAAAGCCAAANGGAG
CCGGCGCTAGGGCCTGGCAAGTGTACGGGCACGCTGCGCGTAACCACCCACACCCC
GCCGNGCTTAATGCCCCNTTCAGGGCGCGTNCTGATGCCGNATTTTNTCTTACNCA
TNTGTGCNGGNTT

Sequence ID 833

TAAAATAATGGCAAAAAACAAACAAAAAACAAGTTCTCTAAACAGAAAGGAAATTA
CTAAAGAAGGAATCTTGAAATAACAGGAAAGAGGAAATACCACAGTAGGCAACATT
ATGGGTAAATAAAACAGACTTTCCTTCTTTAGTTTCCTAAAATATGTTTGATGATT
AATGCAAAAATTACAATATTTTCTTATGTAGCACTAAAGGTATGTAGAGAAAATAT
TTAAGATAATTGTACTGTAAGCGGGAGATGACAGTGACATAAAGGCAACGTTTTTA
TACTTCACTCAAACTTTATGTATTAATGTAATCCATAAAGCAACCAAAAAAGCTAT
ACTAAGTACATTCAAAAACACAATAGATAAACCAAACAAAATTCTAAAGGATGTAC
AAGTAACCCACTGGAAGCTGCAAAAAATGTAAACAGAAACTAAAAACAGAGAATAA
ATGAAAAATTAAAAACGAAATGGCAGACTTAGGCCCTAATATACAAATTATCACAT
TAAATATAAATGGTCTAAATACACCAACTGTAAGACAGAGATTAGCAAAGTCGATT
TAAAAACATGACTCAACTACGTGCTGTCTACAAGAAACTCACTTCAAATATACCAA
GATAGGAAGGTTGAAAGTAAAACGATGGAAAAAGATGTATCATGTGAACATTAATC
AAAGGAAAGCAGGGGTGGCTATATTAACATCAGGTAAAATAAACTTT

Sequence ID - 837 nt: 603

TGAGGNTGGTCATGATGCANAAGCTACTCAAATGCAGTCGGCTTGTCCTGGCTCTT
GCCCTCATCCTGGTTCTGGAATCCTCAGTTCAAGGTTATCCTACGCGGAGAGCCAG
GTACCAATGGGTGCGCTGCAATCCAGACAGTAATTCTGCAAACTGCCTTGAAGAAA
AAGGACCAATGTTCGAACTACTTCCAGGTGAATCCAACAAGATCCCCCGTCTGAGG
ACTGACCTTTTTCCAAAGACGAGAATCCAGGACTTGAATCGTATCTTCCCACTTTC
TGAGGACTACTCTGGATCAGGCTTCGGCTCCGGCTCCGGCTCTGGATCAGGATCTG

GGAGTGGCTTCCTAACGGAAATGGAACAGGATTACCAACTAGTAGACGAAAGTGAT
GCTTTCCATGACAACCTTAGGTCTCTTGACAGGAATCTGCCCTCAGACAGCCAGGA
CTTGGGTCAACATGGATTAGAAGAGGATTTTATGTTATAAAGAGGATTTTCCCAC
CTTGACACCAGGCAATGTAGTTAGCATATTTTATGTACCATGGNTATATGATTAAT
CTTGGGACAAAGAATTTTATAGAAATTTTTAAACATCTGAAAA

Sequence ID - 839 nt: 71
ATTTATCTAATATTTGGTTTAATAAAATGTGAATAATGAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

Sqeuence 849 nt: 622
TTTTTTTTTATTTTTTGAGAATGGAGTCTTGCTCTGCCGTCCAGGCTAGAGTTCAG
TGGTGCGATCTCAGCTCACTGCCACCTCACCTCCTAGGTTCCAGAGATTCTTGTGC
TTCAGCCTCCTCAGTAGTTGAGAATACAGGAACACGCCACCACGCCTAGCTAATTT
TTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTC
CTGGCCTAAGTGACCCACCTGCCTCAGCCTCCCAAAGTGCTGGGATTATAGGCGTG
AGTCATTGTCCCCAGCCGGATGTTTTCATCTTGATTTGCCTTAGTTTCTAAATCTC
ATCCTCTCCATTTTCTCCTGTTAGTAGTCACAGAGAACCAAATTCTGTCAAGTTAT
GAAACTAAAGTCTCTCTTCCACAAGTCTTCCTGTGTTCTGCCTCAAGTGAACTTGA
AAGAACATCAGTTTGTGGGAAGGTTGAAGACCGAATGATCTGCTGGGAAATCACTG
AGGCATTGCCATTCTCTTGAGGAATTTCATTTTCATCGAAGTTTCGGTTTATATCC
CTTTCTTGGTGAGTACTATTGCTGTTATGTAAATTAAATGAGTCGTCATCCTTCTT
NTGAGC

Sequence ID - 860 nt: 501
GTGAAATCACTTTCATGGATTATTAATGGATTTAAGAGGGCATCAATCAGCTCAAC
TCAAGATTTCATAATCATTTTTAGTATTTAGATTGTGCCTCAAAGTTGTAGTACCT
CACAATACCTCCACTGGTTTCCTGTTGTAAAAACCTTCAGTGAGTTTGACCATTGT
GCTCTTGGCTCTTGGGCTGGAGTACCGTGGTGAGGGAGTAAACACTAGAAGTCTTT
AGTACAAAACTGCTCTAGGGACACCTGGTGATTCCTACACAAGTGATGTTTATATT
TCTCATAAAGAGTCTTCCCTATCCCAAGGTCTTCATGATGCCAGTAGCCATATATG
ATAAATTATGTTCAGTGATAACTTAGTTATCAGAAATCAGCTCAGTGGTCTTCCCC
GCCATGATTCACATTTGATGAGTTTTTAAAAATCAAAGTGATTTTGAAAATCTCTA
ATGGCTCAGAAAATAAAAACATCCAGTTTGTGGATGACTATATTTAGATTTCT

Sequence ID 864
TTGTGTTTTTAGGACTCCTTATCTAATTAAGGCAGAGAAGTTACAGTATTTATAT

CTGCATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGA
AACTATTGATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATC
ATTTAATAGGACACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGG
CTGTACTCTAAAATAATATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTC
AAAATGCATACTAATATTTCAATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATC
TACTTGTGATAGCCCTAAGAGCTGAGATAATTATTTCCAGGAGGTTGAATCCCTGA
TTCTTAACTGTTCAGCAATGCATAAGCAAGAGAGAATATGACATAAGAGGACCATT
TCTACATTAGCCATTTTTTTCACAAGATACCTATGTGAATACAGGGCACCTGGGA
GGGTAAGTGGAGGACTATTTCTAACTATATTTATAAGCACATACTGATATTGGTGA
ATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGACAATGTGTAAGGAGAT
CAGGAATTCATTAG

Sequence ID - 865 nt: 122
CCANAATCCACTCTCCAGTCTCCCTCCCCTGACTCCCTCTGCTGTCCTCCCCTCTC
ACGAGAATAAAGTGTCAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

Sequence ID 867
TTTTTTTTTTTTTTTTTTTCAGAGTCACAGATATTGTATAGCTGAGGTAAGCATTT
TACAACTTTTCAGACACAAGTAAGTACATAAATATTATTTTACAACCAACAATNTT
TAATATTTCCACATTGAANAATAGATGTGATAATTAAATCTTTTATAAGGTTTTAA
AAAGACATGAAACATAAACCTAATTATACATAAAAGAAAAGAATTTTAAACAAGAG
CTTATTGNGATGACATTACTCATAACTTTTACCTTTAAAACCTTTTCTTGGGTAGC
TATTCAAAAGTAAAGACCACAAGTTTTGTTGCCCANATTTCTTATGTTTNGTATAT
TTAAGCTCTTTATTTATTGAACAGATGNGTCATTAATTCATTNGGAGCATTACTAT
TATCAGTAAAATTTGATTTTTTTTCCCCTCAGTCATAGGTAAATCAGCTCCACCT
GGAATTTCTAAGGACCCAGTTTTAGTCAATATTTTCAAGTAATCATGACCTCAGAA
ATAGTCTTAATTAAGATAACAAATATTAGCCATCAAAATGGAACCAAGACAAGATT
CTAATGTTTGTAAACAGTCAATCCATATTTATGAATATTAGCATATATTGGNGAAT
AGTTAAGGCAAAAGGGTCTAGCAG

Sequence ID - 869 nt: 667
TTGTGTTTTTAGGACTCCTTATCTAAATTAAGGCAGAGAAGTTACAGTATTTATAT
CTGCATTAAATCTCAATTCCAGAAAAACCTTTTGAAAAATTATTTAATCCTCTGGA
AACTATTGATATGATACAGGAGAAATTTTCAGAAGTTTATTGAATAATTTAATATC
ATTTAATAGGACACTCTGGCTTGTATATAAGCAGATACGTTACTCAGACTTCTTGG
CTGTACTCTAAAATAATATATGTACTAGTCTCCTAAATATTACTAGCTCACCTTTC

AAAATGCATACTAATATTTCAATGTCTTTCTTCAATTTGAAAAGCTCTTGAATATC
TACTTGTGATAGCCCTAAGAGCTGAGATAATTATTTCCAGGAGGTTGAATCCCTGA
TTCTTAACTGTTCAGCAATGCATAAGCAAGAGAGAATATGACATAAGAGGACCATT
TCTACATTAGCCATTTTTTTCACAAGATACCTATGTGAATACAGGGCACCTGGGA
NGGTAAGTGGAGGACTATTTCTAACTATATTTATAAGCACATACTGATATTGNTGA
ATCAAAACCTACAGCAGTGCTTCTCAGATGGGAAGGGAGACAATGTGTAAGGAGAT
CAGGAATTCATTAGTCACCTTTCAGATGGTTTAATGCATACAGCTGTACCG

Sequence ID 870
GGAGTTTGAGCAGATCCTTCAGGAGCGGAATGAACTCAAAGCCAAAGTGTTCCTGC
TCAAGGAGGAACTGGCCTACTTCCAGCGGGAGCTGCTCACAGACCACCGGGTCCCC
GGCCTTCTGCTCGAGGCCATGAAGGTGGCTGTCCGGAAGCAGCGGAAGAAGATCAA
GGCCAAGATGTTAGGGACACCAGAGGAAGCAGAGAGCAGTGAGGATGAGGCTGGCC
CATGGATCCTGCTCTCCGATGACAAGGGAGACCATCCCCCACCCCCGGAGTCCAAA
ATACAGAGTTTCTTTGGCCTATGGTATCGGGGTAAAGCTGAATCCTCTGAGGATGA
GACCAGCAGCCCTGCACCCAGCAAGCTAGGGGGAGAAGAGGAGGCCCAACCACAGT
CTCCAGCTCCTGATCCGCCCTGTTCTGCCCTCCACGAACACCTTTGTCTGGGGGCC
TCAGCCGCCCCAGAGGCCTGACTTAGGGGTCTGGCTGTGGAAGGATGTGTGGCCTC
AAATGAGGACAGGGCTCCCGCCTTCACAGCCCTCGCCAGGGGTCTGCCCCAATCCT
GGCCTGCATCAGGCAAGGACGGGGTCTCAGC

Sequence ID - 871 nt: 642
GCAAGTCTTCAGTATGTACATTTATCCCCTAGAAGAAGAAAAATTAGTTGTGCATG
AAAAAGAAACATTAACTGCAAAGCTAAATGCTCACACTCTAAATCAGTGCTCTCCA
AAGTACAGCAGGCGGGAAAAGAAAATGGTAGATTTTTTCTTCCAATTACTTTAAC
TTATTCTTTTTAATGGACACTTCATACATAAATATATTCACAATATATTAATATAT
ACATAATGTATAAGCATACATATTGAATGTGCAGTCAAAAAATGTACTAATGGAAT
GCTCTACCAAAACAAGTTCACGTTCATCTGTAAAATGGGAATAATATTTTTAAAAG
GCATACAGTCTGAACATTTTTAGATTATTCATAAAATCTATTCAGAAAGTTAAACT
AAAAAATTTAACGTATGCCTATAACAAATTTTGTACTTAATGTAATTGNTTTTCAT
CCTGAGATCTAATATCCTCGTTTTTAAGTAGAGCCACTTGTTTGCTACAGTTTAGT
CAAAACGTTAACATTAGATGGGTAAAGTAATATGAAATCTTTCTACTACTCCAAAA
TAGAAAACAGAACATTAAAAAGATAAAAATTCAAACATACTTACCAGTAGATTTTC
AACTGNGCAAAAGCTCATTGCATGGG

Sequence ID 873
GTTTTCCACCGTGAAGAGAACATTTCCTCTGGGAATGACAAAGCCCTCAGGAACNG

CTTTTATTTCTATTGGAAGATGCCCATCATACTTCTGGCAGGATAAAATGATAAAT
TTATTTATTCAACAGATGATACTCAATTCCCTGCTGTTTTACTAAAGGTTCTTTAC
GTTTTATAGAAGCTAAATTTACTGTCATAGAAATTGCAATTGTAGATGTTACTGTA
ATCTAGTCAGAATATCCTTATCCTTCTAAAATAAAACTAGTTAAAATTATTAACAT
ACGTACTGATATTAATTTTTAAGTTTAATGCTGCCACGTGCTTCTGCTAAGAACAT
TTATCACTACAAGTGGCAGAAAATTCCAAACTCATCAAAACCAAACTGTTGCTTCT
TCCCTGCTTTTTCAGAAAATGAGAAAGGATGACTTTATTCCAACATATTCTAAAAG
TATTCCAAGAACACTACCTTTATTCTAAATTCGTTATTTTCACAAAATAAAGGCTG
CAGATTGAAAGATAAAGGATTGCTATTAAAGAACAAAAGAAAACAAAACCGAGAGA
GAAGGAGAGCTAGGGAAATCCCTGCANAANAACCGAATANGGTCCCTCTATTCTGG
GCCGGGGCCTGAAACTATGAAACAGGCCAACACAGAATCTTGGCA

Sequence ID 875
CCTCTGACTCGCTCAGCTCACCCACGCTGCTGGCCCTGTGAGGGGGCAGGGAAGGG
GAGGCAGCCGGCACCCACAAGTGCCACTGCCCGAGCTGGTGCATTACAGAGAGGAG
AAACACATCTTCCCTAGAGGGTTCCTGTANACCTAGGGAGGACCTTATCTGTGCGT
GAAACACACCAGGCTGTGGGCCTCAAGGACTTGAAAGCATCCATGTGTGGACTCAA
GTCCTTACCTCTTCCGGAGATGTAGCAAAACGCATGGAGTGTGTATTGTTCCCAGT
GACACTTCANAGAGCTGGTAGTTAGTAGCATGTTGAGCCAGGCCTGGGTCTGTGTC
TCTTTTCTCTTTCTCCTTAGTCTTCTCATAGCATTAACTAATCTATTGGGTTCATT
ATTGGAATTAACCTGGTGCTGGATATTTTCAAATTGTATCTAGTGCAGCTGATTTT
AACAATAACTACTGTGTTCCTGGCAATAGTGTGTTCTGATTAGAAATGACCAATAT
TATACTAAGAAAAGATACGACTTTATTTTCTGGTAGATAGAAATAAATAGCTATAT
CCATGTACTGNAGTTTTTCTTCAACATCAATGGTCATTGNAATGTTACTGATCATG
CATTGGTGAGGNGGTCTGAATGTTCTGACATTAACAATTTTCCAT

Sequence ID - 876 nt: 115
AAACTTTTGTGGCAACAGTGCACTAATTTGGATAATGTTTGTTCCCAATAAATTAA
GAGCCAAATTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

Sequence ID - 878 nt: 634
GCCAGGCTTTGTGAATTACAGGACATTTGAGACAATCGTGAAACAGCAAATCAAGG
CACTGGAAGAGCCGGCTGTGGATATGCTACACACCGTGACGGATATGGTCCGGCTT
GCTTTCACAGATGTTTCGATAAAAAATTTTGAAGAGTTTTTTAACCTCCACAGAAC
CGCCAAGTCCAAAATTGAAGACATTAGAGCAGAACAAGAGAGAGAAGGTGAGAAGC
TGATCCGCCTCCACTTCCAGATGGAACAGATTGTCTACTGCCAGGACCAGGTATAC

AGGGGTGCATTGCAGAAGGTCAGAGAGAAGGAGCTGGAAGAAGAAAAGAAGAAGAA
ATCCTGGGATTTTGGGGCTTTCCAATCCAGCTCGGCAACAGACTCTTCCATGGAGG
AGATCTTTCAGCACCTGATGGCCTATCACCAGGAGGCCAGCAAGCGCATCTCCAGC
CACATCCCTTTGATCATCCAGTTCTTCATGCTCCAGACGTACGGCCAGCAGCTTCA
AAAGGCCATGCTGCAGCTCCTGCAGGGACAAGGACACCTACAGCTGGCTCCTGAAG
GAGCGGAGCGACACCAGCGACAAGCGGAAGTTNCTGAAGGAGCGGCTTGCACGGCT
GACGCAGGCTCGGCGCCG

Sequence ID 879

GTTGCCGGGTCCTGTGATAACTCTGTTTAACATTTTGAGGAACTGTTGAATGGTTT
TTCACAGCAGCTGCCTCATTTTTATTCCCATCAGCAGTACTTCTTGGTTCTAATA
CCTCCACGTTCTCGCCAACACTTGTTGTTGTCTGTAATTTCGTTGTTAGCCATCCC
AGTGGGGATGAAGTAGTATCTTACTGTGGTTTTCAGTTGCGTTTCCCTGATAATTA
ATGATGGTGAACATCTTTTCATGTTCTTGTTGGCCATTTGTATGTCTTCTTGGGAA
AAAAAAAATGTCTGTTCAAATCCTTTACAAAGTATTTATTTTTTATGTCAACAATA
TAACCACTCAGTACACTGCTTTTTANACAATGATCTTTTAAAGGTTTGTTTACAAC
ATTTAGCACTTGAAATTTTAAGGTTATGCCCTCAAAAAAATTGCTGAGGGAGCTAA
GCTATGAAGATGCAAAGGCATAANAATTATACAATGGACTTTGGGGGAATCCAGGG
AAAGGGTGGGAGGGGGGTGANGGA

Sequence ID 881

TCGACTCTGATTTTTTTTTCTCCTTCCTCGCAGCCGCGCCAGGGAGCTCGCGGNGC
GCGGCCCCTGTCCTCCGGCCCGAGATGAATCCTGCGGCAGAAGCCGAGTTCAACAT
CCTCCTGGCCACCGACTCCTACAAGGTTACTCACTATAAACAATATCCACCCAACA
CAAGCAAAGTTTATTCCTACTTTGAATGCCGTGAAAAGAAGACAGAAAACTCCAAA
TTAAGGAAGGTGAAATATGAGGAAACAGTATTTTATGGGTTGCAGTACATTCTTAA
TAAGTACTTAAAAGGTAAAGTAGTAACCAAAGAGAAAATCCAGGAAGCCAAAGATG
TCTACAAAGAACATTTCCAAGATGATGTCTTTAATGAAAAGGATGGAACTACATT
CTTGAGAAGTATGATGGGCATCTTCCAATANAAATAAAAGCTGTTCCTGAGGGCTT
TGTCATTCCCAGAGGAAATGTTCTCTTCACGGTGGAAAACACAGATCCAGAGTGTT
ACTGGCTTACAAATTGGATTGAGACTATTCTTGTTCAGTCCTGGTATCCAATCACA
GTGGCCACAAATT

Sequence ID 883

TCATTTACATTAATACTCAAAACTGCTCGATTAAGCAGGTGCTGTTCTTATCGCCA
TTTTGCATATGATGAGAAAGGGTAAGGTCACCCAGCTAGTATTTGGCTCACAGCAG
GCCTTAAGACTTGGTTTGTGTGACTCATCAGTCCACGCTCCTAAAACCACTAAGTT

GTTCTACCCTTTAATGTTGAATTAACATTGGATAGTGTTCAAGTTTANATGGGTGG
GTGAGGGCCCAAGGACCTTTCAAACTCAGATCTCTTATTTAATAACCTGGTCCCAG
ATCCATTCCTCTGTCGAAGAGGAAGTCATCCTTCAGTGGCTATTCATTGTGGGGTT
AAGAGCGCAGACTATGAATTCAGTCTTTTTGGGTCCCAGTTTGCCAGACCTTGAGT
GAGTGCCCCGAGTTTACTTACTTGTAAAGGTAGGTGGAGGTAATATAATTAAATAA
ACTTAAAAAACTAATTAAAAACAAAACAAATGAACTAAGGTCTTAGGATATCTGGC
GTCTATTTTGCGCCAAATCACATAATGTCTATTGTTGTGTGTTGGACTATAGGATT
GTCCTTTAACAGGGAAGGGTTTATTTCTGTAATCAAGTCTGTCAATATTATGACCA
TGTTGATAATAGCTACCTTTAATTGAGGGCTTCCATGTGCCAA

Sequence ID 885

TCAGTGGAAAAGGGCAGGTTGAATCAAGGTGAATCAATCTGAAATTGAGCACACCT
GCCTGCCATCGCTGTTCCTTCAACTGAGTGCTGCACATCATGGGCTCTGTCTGTGA
GAGAAAAATCCCGGTGCTTGGTGTCCTTGCATGACATGGAGTTTTGCATGTAGATC
AATTTAAAATGTACCTCTTGTTTACATAATTTGCATAATTTTAAAAGATAATGTTG
CCAAACTTTGGAAATGTTAATGTTCANACTGAAAATCTCCACTACATGTAACTTTC
TTCCTCTGGATCAGTGGCATGGCTTATAATCCCAGCCAGTGGTTTGAACTGTTCCA
GTGTCAACTGCCATGTGCTCTGCTTCAAGGGGGAACTAGCCTTTTGTGAATTTTTT
GTACATAAGTATTTGTTACAAATATTTTAGCAAATGCTTTCTATTTCTCTTGCTTG
TGCATATCTTGGCTGGCGTTACAGAAAAATAGTGTAAACATTATTTCCTTACCGGG
GAATGAGGGTTTT

Sequence ID 887

AGCACCTGGCACAGAGTAGTAGCTAACACAGATGTTAATTTTGCTGCGTCAAATGT
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CTGTTTTCTCTCCCTGACCTTTACTGTTTGTTTAGAAAAAAAAAAAAAAAAAAAAA
AAAAAA

Sequence ID 889

CAGAGAGCTTGTTCCCTCCCTCCCTGTGCATGCAAACAAGAGGGCATGGGAGCACA
CAGAGAGATGGCAGCCACCTACAAGCCAAGAGGAGAAGCCTCACAATCAAACTCTC
GCTGCTGGCGAGAGTCTTGGACTCTGTCTTGGACTTCCAGCCTCCAGACTGTGAGA
AACAAATTTCTGTTGTTTCAGCTTCTCAGTCTCTGGTGTTTTGTTATTGCAGCCTG
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AATGCAATTATTTATTTGCTTTTCAGTCTCTACAAAACGTTCTAAAACACTAATCT
AAATATTAACAGTAAAATATTTGCATAACTAATGGAAACTAAGAAATCATATGACC
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CTGGGCTTGAAATTGCAGGCTCTCCTAACTTAAGCAAAATCTGACAGATCAGCAAA
ATGAGATAAATGTTTCTTTTTTCTTTCTGACTGCATTAAATCAGATACAACTCAGC
ATTAAAAAGCTATCTTTGNAAAATGNTGGTACTAATAAATTAGTCTTA

Sequence ID 890
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AGATGCAGATACTGTCTCCATGAATCTTATAGGCTAGAAAGGAAATAGATAAGTAG
TCCTACCAGAAGAACATGATGAAGGCATTTGTGGTAAACAGAATGATGGCCCCCCA
AAGATGTCCACATCCTAATCCCTGAAGCCTATGAATATACTACTTTACTTGGCAAA
AGGGACTTTGCCACAGGTTTTTAATTAAGGACCTTGAAATAGAGAGATTATCCTGG
ATAATCCAGATGGCCCCAGTGTAATCCCAAGGGTCCTCACAAAGGGTAGGAAGGAG
AGCCAGAGTCAGAGAAGGAGACGTAGCAATGGAGGCAGAGGTCANAGAGAGATCTG
CAGATGCTGCTGTGTTGGCTTTGAAAATGAGGAATGCAGGTGACCTCAANGNGCTA
GATGATGCAAGGAAACAAATAATCTCCTATGAACCCTAGGATGGGCATTATTATGA
GTCCTATTTTATAAACAAGGAACTGACNTCCAGAAAGATAAATGC

Sequence ID - 891 nt: 626
GGCAGAGGTTGCAGTGAACTGAGATCATGCCATTGCAATCCAGCCTGGGCAACANG
AGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAGACAAGAGTNTCCACTCTAAACA
CTTNTATTCAACATAGTCCTGAAAGTCGTAGCCACAGCAATTTAACAAGATAAAGC
AATAAAATGTATTCAAATAGAAAAAGAGGAAGTCAAATTATCTTCACTGGNGATAT
AATTCTCTACCTGGGAAACTTCACCGAAAAAGATTTCACCAAAAGATTTCTAAGCC
TAAATAATGACTTCAGCAAAGTCTCACCATACAAAATCAACATACACAAATGAGTA
GCATTTCTGTGCACCAATAATATTCAAGCTGAGAAAAAAAGAACATGGTTCTATTT
ACAATAGCTACAAACAAAAAAATATGTACCTAGTAATACATTAAATCAAGGNGGTA
AAATATCTNTACAACAAGAACTACAAAACTGCTGAAAAAAAATAGAGACACGCAAA
TAAGTAAAAAGGCACTCCATGCTCATGAATTTAAAGAATCAATATAATTAAAATGT
CCGNGCTGCCTAAAGCAACTTACAGATTAAAGGCTATTTCTCTCAAACTATAAATG
CACCTTTTTA

Sequence ID - 893 nt: 585
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CTCCCCACATACCTTCCCACACTCATCACCTTAAGCCAGACTCGGTGTCCAGTGAA
TATGACCATCTCTTGCCCATTTTCTAATGAGTGTTTTCATTAATGAGTTATAAGAA

TGTGGTGGGTAAATCTATGGGCTTTGAACTAGTGAATCAACTTGGTTTCAGAATCT
GGCACTGCTACTTACTAGTGAATTTAAGCAAGTTATTTCACCTTTCAGAGTGTCAG
TTCCCTCATGCATACAAGGAAGATAAAAAATAATGTNTACNAAAGTATTGGAGTAA
TTAATACATGGAGAACTACATGTAAAGCGTTTAGCATGATGTCTGACATATTAAGC
ATCCAATATTAGTNGCTTGCAGAATTATTAGTAAAAGAGATTGCTTCTGAAAGCCA
TTCCAATTCTTAAATTTTATAATGCCACATTTGAGGTCACCTGAAGTCGTGTATAA
CATGTGTACATTTTTGCGATTTATTTTTTCAATTCCCANATTAAAGGCATAGAGAT
ATCCTAGCNANGGACTCCAAGTGTG

Sequence ID - 895 nt: 560
GTAATTGCAGCCTGGGCAACGGAGTGAGAGACTGTCTCAGGAAAAAAAAAAGAAAA
AAAACTACTGAGGTAGTTGAATATATCCTCCATTCCCCATTTGTGGATTAGTTAGT
AAATGGGGCATCTTAGGGTTTAAATATGTCCAGGGTCACTGAGGATCAGATCCTAG
GGTTCCTTTGACTCAAGGCTTTTGTCTCAGCAAAACGTCACCTTCCAGCAGGAAGG
CTTTCTCAGGCAAGTAGCAGGGTGGCTACTATGTATCGCTTCTTTATTTTTTCTTT
TTTAAAATAATGCAGGCACCGTGCGCATAATTTAAAAAATCAGTGCTAAAACCCTT
AAAAAAAAAAAGCTGTTCTCATCTCCTGTCTTTCTTTTTTTTTCTTTTTATTTTT
TTCTTTTATTATTATTATACTTTAAGTTTTAGGGTACATGTGCACAACGTGCAGGT
TTGTTACATATGTATACATGTGCCATGTNGGTGAGCTGCACCCATTAACTCGTCAT
TTAGCATTAGGTATATCTCCTAATGCTATCCCTCCCCCCTCCCCCCTTTTTTTTT

Sequence ID 896
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GTTAATTATCTACCTTTCANAAACTGGAANAAGGCCTAGCCTAGAGCATTGAAAAC
AATAAGGGAAAGGAGGAGTAAGGCTGGANAGATAGGAATGGTTTAAAGTCTTTGTT
AAAAATTTTTTTAAAAAAATCTTTATCACAAGAAGAGGATTGGCNTGATCAAATTT
GACTTTTAAAAANATTACTTGGGTTGGGCATGATCAAATACTACTTAGGGAGATTA
GTTTANATGATAATGGCATTCTGGACCANAGTGGAGTCAGAGGTGAAAAGAGGTAG
ATATTCCANAATTGAGGGATTTGTGAGGTGAAATCATTTGTTACAGATATTAAAGG
ATAAGGAGCTTTGTCAAAGGGGATCTTAAGTTTCTGGTATGGTAACTGGGTTAGAG
AGCCCTGGAACATGACCAGCTTTAAGGGAAGAGAGCTTGAGCTCTGTTCTTGTTAA
GCTCAGTTTGAGATCTTTGTGGAATCAAGTGGAGAGGTCTAAGCAGGGAACTGGCT
TGGCTAGGCTGTAAAGATGAATCTGAGAGTCCCAAGAATATGGTAATTATTAATAA
AAGCCTTAGGTANATGAAATTGTTTTGGG

Sequence ID - 897 nt: 509
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AATGCTAGTTTCTTGGTTTTGATATTGTACCATAGTTATGTAAGATGTAACCATTG
GGGGAAACTGGGTGAAGGCTACATGAGACCTCTCTGTACTTAATCTTTGCAACTTA
TGTGAATCTATAATTATTCCAAAATAAAAGTTTTAAAGAACCTAAGTATCCTTAT
TACTGAGGGTCATCGTGCTAGACAGCAAGGTTGGGCCAGAGCTTCTAGTTATTTAA
AATACTAAATACCAGCCTGGGCAACATAGCAAGACCCTGCCTCTACAAAAAGCAAA
AAAATTAGCTGGGCATGGTGGTACATGCCTGTGGTCCTAGTTACTCTTGGAGGAGT
CTGAGGTGGGGAGCTTGAGCCTAGGAGTTTGAGGCCGCAGTGAGCCTTGATTGTGT
CTCTGTACTCCAGTCTGGGCCACAGAGCAAGACCCGGTCTCTAAAAATAAATAAAT
AAATA

Sequence ID 898
ANTGCACTCCAGCTTGGTGACAGAGGGAGACTCCATNTTAAAAAAAAAAAAAAAAA
AAAAAAAGGGAGTAGCTTGAAGCCACATAGTAGTTAGTGGTAAAGGCCACCCCTTT
TCCCACAACTCACACCAGCACCACAAGCTAGCCTTTNTAATTTCCAAGCCAGTGCC
CTTTCAACGCACACACCCCTGTGTCAGTTCCCTTTCTGCTGCAAGCTCTCTGGAGG
CAGATACTGTTGAGTCCCTGGCCTGCCTATGAGAACGGCTCATGATCTCTATTTCT
TCTGCTTAATGACCATCTCGAAGTAACAAGTTTAGCCTAAAATAAACTTGCTAAGT
TAGCAAAGGAAGTCCTTAGCAGCCACCATTTCTCGATTCCTCCATCACCTCCCCTG
CCCCTCAACTCCCTCATTTCTCCCAAGATATGGGCTCCAGGCTGGGCGCGGTGGCT
CACGCCTATAATCCTAGCACTTTGGGAGGCTGAGGTGAGCAGATCACTGAGGTCAG
GAGTTCG

Sequence ID 899
TCNTTCGGAACGCGCC

Sequence ID 900
CTGGAGGGATGGGTAGGATTTTGACAAGAGTGGTTGAAGGTATTCTAATTCACTTA
GTACCTACATGTGCGAGGCAGCATGAAGGCAAAAAAGCCTGGGGCATGTTCAGAGA
ATAGCAAGTATTCTAGTTTGAGTGGCACCTGGTACGTATATAAGGGAATAGTAAAA
GATCTGGCTGGAAAGGAAAAGTAGGGGCAGGTTACGAAGGACCTCTGAAAGTCAGA
CTGTGGAACTGGAACTTTTATCAGGAAGCAGTAGTTAGTTTTTTCAAGCAAAAGCT
AATTAGAGTTGATATTTAGGAGGATGAATCTAACAGTTGTGTGCAAGGATGCCTTC
AAACTGAGTGAGACTAGTACTGGAGACTGGTTAAGAGACTACAACAATAACCTGAG
TAAGAATTAATACAGGCCTGACCTAGTTTTGAGTGAGTAGGATTGGAAACAAGAGT
TTTAGGTATTATAGGATTTATGCATATAAAATGGACTTGACAGAACTTGAAGAAAG
AGAAAGTGTCAAAAGGACACAGAAAGTGAGGCAGGATATCTTACAATGTTAAAGGA
AAGGAATAATAGAAGTTAC

Sequence ID 903

GGAAACATAAGCTTGTTTCAGTACACTCACGCTGTAGATTAATTCTGATATTACAT
ATCTCCATCAGACTTTGTACCCTCTCTTCCATCCCTTACCCTTACCGATTAGGT
TGGTATTACCTAAAAATCCATAGAAAATGTCCAGGTGAATTGCCTTATGCTTTCTA
CCCCATAAGGTATAATT

Sequence ID 904

CTCTGTGGTGTGAGAACACAGTGGGTGACCAAGGCTTTCCAGATGAACCCAAGGAA
AGTGAAAAAGCTGATGCTAATAACCAGACAACAGAACCTCAGCTTAAGAAAGGCAG
CCAAGTGGAGGCACTCTTCAGTTATGAGGCTACCCAACCAGAGGACCTGGAGTTTC
AGGAAGGGGATATAATCCTGGTGTTATCAAAGGTGAATGAAGAATGGCTGGAAGGG
GAGTGCAAAGGGAAGGTGGGCATTTTCCCCAAAGTTTTTGTTGAAGACTGCGCAAC
TACAGATTTGGAAAGCACTCGGAGAGAAGTCTAGGATGTTTCACAAACTACAAAGC
TGAAGAAAATGAAGCCCTATTACTTGTTTGTAAGATTTAGCACCCTTCTGCTGTAT
ACTGTACTGAGACATTACAGTTTGGAAGTGTTAACTATTTATTCCCTGTTAAAATT
TAACCTACTAGACAATGATGTGAGTACCCAGGATGATTTCCTGGGGCACAGTGGGT
GAGGAGATGGGGACAGGTGAATGGAGGAGTTAGGGGAGAGGAAAAGTGGATGGAAG
TGTCTGGAAAGGGCACCAAAAAAGTCTTCCAGGTCTGATCCTGTTTCTTGCTCTGA
GTGCTAGCTACCACTGTGTCACACTGTAACATN

Sequence ID - 905 nt: 655

CTCAGCTCTTGCCTGGTCACCTTGTGGCTTTTACCATCCTCATCCCCTGTGCCACC
CACATCCTGCCACTTCTGCATGGAGTTGGGGTGGGGCCATTGGAGAAAAGAGGTTA
AACAAGCAGTAATTTACTTGAGTACAGTCTTTGAGCCAATGAAATGCCAGTCATCA
TTTCCCAGGGGTACTTGTCATCTTGTCAACAACCCGCTGATAATGCTCCTTCAATG
TGAATAGCAAAAGTAGGGAGAGACGCTGAATGAAGAAGATGCCTACCCCTCAGGAA
GACTGCTGTCCGCCTCCAGGCCTGCATGCACACACCCATGCCCACCTGCACCCCCA
GCACCACGCCCACACTCACTCGCACACACCCACATGCCAGTGTTTTGGGGTTGGCA
GCCTGGACACTGCTGAGGCAAACACAAGTCATCAAGCATAATTCTCATTCTCTCCT
TCTGTCTCTGTTTTAGTTACAGGAATTTGGTCAGTTTAGAGGATTTAATAAGTCCG
TGGAAAATTTGTTTCTGTCTCTTGCTACCCACGTGAAAAGTAAGTGCATGCTTCAT
GATGTGTTTTCCCACTACCTTCCAGGCCAGCCGAGCCCACTGGCCANGGCCTGGCC
CGGTGACCTCGGTTGACACTGTCCTCANGCCACTCACTT

Sequence ID 906

CAGAATTTCATGTTTATGCTGCACAAGGCCTGTATTTTATAATGGTGGCTCTTTTG
GACGATGACTTCCTCGATGGTGAAACTTCCAGTAATCTCCCTCATCATACTGAAAT

GATATCAGTATATCATCAGAACACCATGGAGCTTGTCATTTGAGGGACACAGCTTG
CTTGTGTGCTTGGGAAAGAAGAGGTTTAGCATGGTTTCAGGTCAGTGATGAGTCCA
ATGATCTCTGCAAGTTCCCTTAGCTCTGANAATTCTGATGTCATATGCACTTCTGC
CGCCAGAGTTGCTGCTTACTGGATGCGTAAGAAGAAAAGAAAAAAAAAAAAAAA

Sequence ID - 907 nt: 582
CTTCCATTGGGGGTAAAGATCAAACTTTAGGCGAGCCAGGTCTGTATCTCCATTCC
TGTCTCTGACTGCTTCCCTGTAGGGATTGTCTGCAAGCGCACACCTGCATTTTCTT
GTCCACAAGTCTATGCTCTAACTCTGTCACCTGCATGGCTGCAAATTAGCTTCCTT
CTTCCTGCCCTCTTCTCTCTAGCTTGGATTTTGAATTTGAATGGCAGGCATGGGAT
GTCCGTGTGTGTGTACTGCTGATGTGTACAGCCGCTTGTTAGCGCTCTCATTGTCT
TCAAATGTAAGTCATTTTGGCTGGGTGCGGTGGCTCATGCGTATAATCCCACGCTT
TGGGAGGCTGAGGTGAGCTGATCATTTGAGGTTAGGAGTTCGAGACCAGCCTGGCC
AACATGGCAAAACTCCATCTCTACCAAAAATACAAAAATTAGCTGGGTATGGTAGT
GCACGCCTGTAATCCCAGCTACTTGGAATGCTGAAGCAGGAGAATTGCCTGAACCC
ANGAGGCGGAGGTTGCGGTGAGCCAAGATCACGCCACTGCACTCCAACCTGGGTGA
CAGAGCAAGGCTGTGTCTCAAA

Sequence ID 908
ACCTGACTTCAAACTATACTACGAGGCTACAGTAATCAAAACAGCATGGTACTAGT
ACAAAAACAGACCAATGGAACAGAATAGAGATCTCAGAAATAAAACTGCACATCTA
CAACCATCTGATCTTCAACAAACCTGACAAAACGAGCAATGGGGAAAGGATTCCCT
ATTTAATAAATGGTGCTGGGAGAACTGGCT-AGCCATGTGCAGAAAATTGAAACTG
GACCCCTTCCTTACACCTTATACAAAAATTAACTCAAGATGGATTAAAGACTTAAA
TGTAGAACCCAAAACGATAAAAACCCTAGAAGAAAATCTAGGCAATATCATTAAGG
ACATAGACATGGGCAAAAATTTCATGATGAAAACATCAAAAGCAATGGCAACAAAA
GCAGAAACTGACAAATGGGCTTCTGCACAGCAAAAGAAACTATCGTCAGAGTGAAC
AGACAACCTACAGAATGGGAGACAGTTTTTGCAATCTATCCATCTGACAAAAGTCT
AATATCCAGAATCTACAAGGAATTTAA

Sequence ID 910
CAAAAAACAAGAATTACCCGGGCTTGGTGGTGCATGTCTGTAGTCCTATCTACTCA
GGAGGCTGAGGCTGAAGGATCACTTGAGCCCAGGAGTTTGAGGCTGCAGTGAGTGA
GCCATGATCATGCCAGTGTACTCCAGCCTTGGCAGACTGAGCAAAACTTGGTCCCT
CGCAAAATGTTGAAGCCCAGTTTTCACTATTAACCTGTATTTCAGTTTCCCCATGC
TAACTTTGAAACACTGGGGCTGGCCTGAGGGTATAAAGGCTTATTCAAACTCAGTA
ATTTAAACTTAAAATCCTAAGGAACTTCAAAAAGTGTAATCTAGTCCAAATGGGGC

ATCAATTCTAAAGCATTTGCTTGTTTGAGCAGATTTTCTGTGTCTGAGGTATATAG
ATAACTTATCTTTTTATGACTAAATCCAAGTCCTTAGTTCCTGTTGGAATTCAAAA
TCATATTTAAAAATTGATGCTTTGTTCTATAATTAATGCTTTGATTGTATAAATAA
TAAGTATTCTTCCAAATCCCTTTTTACAGATGATGATTCTGATACCGAGACGTCAA
ATGACTTGCCAAAATTTGCAGATGGAATCAAGGCCNGAAACAGAAATCAGAACTAC
CTGGNTCCCAGTCCTGTNCTTAAAATTCTAACTCGAC

Sequence ID - 911 nt: 595
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AAAGCGAAGGAATTTCGCAGAGCTGAAGATCAAGCGCCTGAGAAAGAAGTTTGCCC
AAAAGATGCTTCGAAAGGCAAGGAGGAAGCTTATCTATGAAAAANCAAAGCACTAT
CACAAGGAATATAGGCAGATGTACAAANCTGAAATTCGAATGGCGAGGATGGCAAG
AAAAGCTGGCAACTTCTATGTACCTGCAGAACCCAAATTGGCGTTTGTCATCAGAA
TCAGAGGTATCAATGGAGTGAGCCCAAAGGTTCGAAAGGTGTTGCAGCTTCTTCGC
CTTCGTCAAATCTTCAATGGAACCTTTGTGAAGCTCAACAAGGCTTCGATTAACAT
GCTGAGGATTGTAGAGCCATATATTGCATGGGGGTACCCCAATCTGAAGTCAGTAA
ATGAACTAATCTACAAGCGTGGTTATGGCAAAATCAATAAGAAGCGAATTGCTTTG
ACAGATAACGCTTTGATTGCTCGATCTCTTGGTAAATACNGCATCATCTGCATGGA
GGATTTGATTCATGAGATCTATACTGTTGGAAAAC

Sequence ID - 912 nt: 651
CATTTCCAGAGTTTATGTGAATTGAATTGAACTATGGTTTTATGTTACTGTCAGTA
GAATGAAGTACGAATATTTGAAAAATACACCTTCAACTTCAAAGTGATTCTTGACA
AAAATTATAAGGAATCATTTTGGACACATTTTCTGGTAGAGCCTTGTAAAAATTAA
AACCAAGTGTTGTTTTCAAGAAGAACTGTAATACATAATCAGGAATTTGAGTAGGG
AGATTATTTTGTTATTTAAAATTAAAGTGGCTGTGTAGTTTTAACTTTAGTATTGC
AGGTAGAGTAAGCTTACATGATAACAAAAATCTTGGTCTTAGTGACTTAATGATTC
TGATATTTATTGATTGATTGGTTATCATTCCAAATATTTTAAAAGATAATAGCTGG
CTGGGTGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCAGGACGGGCG
GATCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCGTCTC
TACTAAAAATCAAAAAATTAGCCGGGTGTAGTGGCGGGCACCTGTAGTCCCAGCTA
CTCAGGAGGCTGAGGCAGGAGAATGGCATGAACCTGGGAGGCGGAGCTTGCAGTGA
GCTGAAATCGTGCCACTGCCTCCACCTGGCGACAA

Sequence ID 913
GTGAGGTGGGGACTTCATTCATTGTCCTATTTCTATCTCCACTTTGTGCCTGGAGA
GCTTTCAGGGGAGGTGGAGGAGGAGGGTCTGCCAAGCTACTGCAACATCTGTCACC

CACTATACCCAGTTACTTGGGGGAGGACAGACACTGTGGTGTCATTAAAGTTGTTT
GAACCAAAGTGGCGGCTGCATCTTTGTCCCGATGCTAGCCGTGCCGGTCTCCCATC
ATCCGCTCGCCCTCCTTTNCCCTGGGCTGCGCCCACTTGTCTTCCTGGATATTTGG
GGGTGACTCGCCATGCTTGGCACCCTCTGCTTCCTGGTGCTGCTCTGACTCGAAGA
CGGGACAGTCCCTGGTGCACATCCAGGGAAGAGGAGTGTCGGTAGTTCTTGCAGTA
GGCACTTTATCAGGACCTGACCTGTTGCTGGGTGATTTTAGTCTCTACAAACAGAA
AGCGTTTCAAAGCGTCAGCTGTGGGAGCAGAGTGACCCTTTGCTGATGCTGGGGGG
AGGGGATCTAAATCCTCATTTATCTCT

Sequence ID 914
GGCGCCTGCTGGAGGAGGAGAGAGCTCTGCTGGCATGAGCCACAGTTTCTTGACTG
GAGGCCATCAACCCTCTTGGTTGAGGCCTTGTTCTGAGCCCTGACATGTGCTTGGG
CACTGGTGGGCCTGGGCTTCTGAGGTGGCCTCCTGCCCTGATCAGGGACCCTCCCC
GCTTTCCTGGGCCTCTCAGTTGAACAAAGCAGCAAAACAAAGGCAGTTTTATATGA
AAGATTANAAGCCTGGAATAATCAGGCTTTTTAAATGATGTAATTCCCACTGTAAT
AGCATAGGGATTTTGGAAGCAGCTGCTGGTGGCTTGGGACATCAGTGGGGCCAAGG
GTTCTCTGTCCCTGGTTCAACTGTGATTTGGCTTTCCCGTGTCTTTCCTGGTGATG
CCTTGTTTGGGGTTCTGTGGGTTTGGGTGGAAGAGGGCCATCTGCCTGAATGTAA
CCTGCTAGCTCTCCGAAGCCCTGCGGGCCTGCTTGTGTGAACCGTGTGGACAGTGG
TGGCCGCGCTGTGCCTGCTCGTGTTGCCTACATGTCCCTGGCTGTTGAGGCGCTGC
TTTAACCTGCACCCCTNCCTTG-CTCATANATGCTCCTTTTGA

Sequence ID - 915 nt: 230
TTTGAGACCAGCCTAGCCAACATGGTGAAACCCCATCTCTACTAAAAATACAAAAA
TTAGCCGGGCGTGGCGGCACATGCCTATAATCCCACTTACTTGGGAGGCTGANGTA
GGAGAATCGCTTGAACCCANANAGGCAGAGTTTGCAGTGAGCCGAGATTGTGCCAT
TGCACTCCAGCCTGGGCGACAGAGCGAGACTCCATCTAAAANAAAATAAATGAATA
AAATAA

Sequence ID 917
NNCAGATTTTTTTTTTTTTTTCAGNGTTAGACCATCTTTCAATTCCTGGAACAAAC
TTAACTTTCCATGATATGTATTTTTTATACATTGCTGGATTTTATTTGCTAATATT
TTACTTAGGATTTAATTTTCTAAGTNGACCTATAATTNTCCTGTATAAAATTGCAT
TTGTCACATTTTAGTATCAAGGTTGTCCTANCNCCATGAAATGGATTTANAATGGT
TTATGTAANATAAAGTACATTTCTTCTAAAGGTTTGNGTGGATTAACTTTCAAATC
TGCCANAGNGNGTTTTTTTCCTTTTTTTTTTTTTTCATTTNAAGGGAGNGCAAGT
ANCTTTTCAAATNCTGATTTAATTTTTAAAATATTTNCAAGTNTNTTTANAGTTTT

TATTTNTTNTNGAANGTTAACATTTTTATANAAAANGGTNTTATCTTTTTAAATTC
TTTGACATCAGTTTCTTCANAATTCCTTCTTTTAA

Sequence ID 926
GTCATATCTCTTCCCAGGGAAAGCAGGAGCCCTTCTGGAGCCCTTCAGCAGGGTCA
GGGCCCCTCGTCTTCCCCTCCTTTCCCAGAGCCATCTTCCCAGTCCACCATCCCCA
TCGTGGGCATTGTTGCTGGCCTGGCTGTCCTAGCAGTTGTGGTCATCGGAGCTGTG
GTCGCTACTGTGATGTGTAGGAGGAAGAGCTCAGGTAGGGAAGGGGTGAGGGGTGG
GGTCTGGGTTTTCTTGTCCCACTGGGGGTTTCAAGCCCCAGGTAGAAGTGTTCCCT
GCCTCATTACTGGGAAGCAGCATCCACACAGGGGCTAACGCAGCCTGGGACCCTGT
GTGCCAGCACTTACTCTTTTGTGCAGCACATGTGACAATGAAGGACGGATGTATCA
CCTTGATGGTTGTGGTGTTGGGGTCCTGATTTCAGCATTCATGAGTCAGGGGAAGG
TCCCTGCTAAGGACAGACCTTAGGAGGGCAGTTGGTCCAGGACCCACACTTGCTTT
CCTCGTGTTTCCTGATCCTGCCTTGGGTCTGTAG

Sequence ID 938
TGGCCATCCTTTTCCCCCCAAACACACCCCCTTAACCTATCTCTTGGGACTTAGCC
CGACCCTCCCTCTCATTTCCCATTAAGTCTGAGAGGCAAGAGCTAGGTTAGGCAAG
GAGGTGGTTGGCCAGAGATGGGGAACAGCCAGGTGCCCCAGTCCTCTGATTTTTCC
TCCATCCTGCTTACCACCTCCCTGGGTACTTACAGCCTTCTCTTGGGAACAGCCGG
GGCCAGGACTGGGTCACCTATGAGCTGAATCAGCATCTCCTCCTGAGTCCCAGGGC
CCCTGCAGTTCCCAGTCTCTTCTGTCCTGCAGCCCTTGCCTCTTTCCCACAGGTTC
CACTTTATATCCACCTTTTCCTTTTGTTCAATTTTTATTTTTATTTTTTTTATTAT
TAAATGATGTGGTCTATGGAAAAAAAAATAAAAATCTGACTTAGTTTT

Sequence ID - 939 nt: 513
GGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACAATGTAGGTTACTAGT
GAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATAAAACAAAA
TTCTCTAACACTGCAAAGAGTGAGCCATGCCTGTTAACACTGTAAAGAATGTAACA
TGTGGGGGACACACAGGGGCAGATGGGATGGTTTAGTTTAGGATTTTATTAGTGCA
TGCCCTACCCTCTGGGGGAACGTCCCATCTGAGGTTTTCTTCTCGGTGGGGGGATT
TAACTTCTGTCCTAGGGAAAACAGTGTCTGATGAGGAGTGTTTCCAACACAGGCTA
CATGAATTCCCCTATACCAGTGCGAAAGCAGCCAGGAGTCCCCGTTGGAAAAGAAC
AATGCCACTCTCTTTTATGTATCTTGGTTCTGCAACTCATTTGTTGTAAGTAGGGT
TAATCGAGTATCAGGTTCACAGTATCCTGCCCTTATTATTTTATGATTCACTGACT
CAAGTTCCA

Sequence ID 947

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AAATTCAATGGGAAAAGTTTAATAAGAGGATTTGGTATCAACTGGCTGTCCAAAGA
TAAAAATGGACCGTCCTATCACATACAAAATTGTTTTTAGATAAAGATTTAAATA
CAGGCACTCCTTCATTTGCGTGGTGCACCTTGAGGTGTTGCAGAAATGATGAGAGC
TGAAACTGCAAAGCAATTTTAATACTTTATCTGTTGGAAATCTTATAGTTTTCCTG
TGACCGTTAAAATTTTCATTAAACTATTAAAAACACCCATGACTGGTCACAAATGT
ATTGGGAAATGGAAAAGAATTAATACACTAAAAATACAAAAAATAGAAAATATTTA
AAATTATCTAAAAATTTGAAACATTAGAAAAATTGAGAACTAGGCAGGGCGTGGTG
GCTCACATCTGTAATTTTAGCCCTTTGGGAGGCTGANGCAGGTGGATCACCTGANG
TCAGGAGTTCGAGACCAGCCTGCCAACGTGGGGAAACCCCGTCTCTACTGAAAATA
CAAAAATTANCCGGGCATGGTGGCACAAGCCTGTAATNCTTGCTNACCAGGANGCT
GAGGCAGGAGAATCACTTGAACCCANGANG

Sequence ID 949

GTTTCACATGAGAAGGTAGTATTATGTACAGTGACCTTGTTTAAAGTGTCNGTTTA
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GTGGAGTTCAGTCCATGCTGGTAACTNTTGAGTATTCAGTGGGTCTTTTAACAATT
ACCACCGTGGAGGANANAGCAAGGAAGAGAAATGCTGTGATCTTTTNCTGTTTTTA
ATTAGNGAAAGAGGGATTANATTAAACAAATGTTACAGAGNTGTGACTNTGATCCC
CCAGNGGTAAGCAATAATTGTANAGACTGGATTTNANAAGCCCTGAGAGTTTATTT
TCAACCTATNTATTATAGNNCAATCC

Sequence ID 1028

ACAAGGCTTGGGGGCTGGACTCCCTCTACTGCCTCTGGCCATACCCCCTCCTGGAG
ATGGGGTCAAGGCACCAGGACTGA

Sequence ID - 1056 nt: 435

TCGCTTGTAAAGCCTGAGACAGCTGCCTGTGTGGGACTGAGATGCAGGATTTCTTC
ACACCTCTCCTTTGTGACTTCAAGAGCCTCTGGCATCTCTTTCTGCAAAGGCATCT
GAATGTGTCTGCGTTCCTGTTAGCATAATGTGAGGAGGTGGAGAGACAGCCCACCC
CCGTGTCCACCGTGACCCCTGTCCCCACACTGACCTGTGTTCCCTCCCCGATCATC
TTTCCTGTTCCAGAGAAGTGGGCTGGATGTCTCCATCTCTGTCTCAACTTCATGGT
GCGCTGAGCTGCAACTTCTTACTTCCCTAATGAAGTTAAGAACCTGAATATAAATT
TGTTTTCTCAAATATTTGCTATGAAGGGTTGATGGATTAATTAAATAAGTCAATTC
CTGGAAGTTGAGAGAGCAAATAAAGACCTGAGAACCTTCCAGA

Sequence ID 1071

NGATATAGTNCCGCATGGGAAAGATGANCAGGTATAACCNAGCNTNATATAGCAAG
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AGCCAAAGCTAAGACCCCNGAAACCAGACGAGCTACCTAAGAACAGNTAAAAGAGC
ACACCCGTCTATGTAGCAAAATAGTGGAAGATTTATAGGTAGAGGCGACAAACCT
ACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATT
NGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAA
CAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCC
ATAGTAGGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACT
ACCTAAAAAATCCCAAACATATAACTGAACTCCTNACACCCAATTGGACCAATCTA
TCACCCTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGC
ATAAGCCTGCN

Sequence ID - 1074 nt: 689

GGGAGGCGGAGGCTGCAGTGAGCTGAGATCGTGCCACTTCATTCCAGCCTGGGCAA
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TTTAAAGCTTGTCATTTTTTATTTAGTAATAACACTCATTAGTGTAGTATCTATGA
TGAACCAGGTTCTGCACAAAGTACCTTATGTTCATGGCCTCATATCGTCTTCTCCA
AAACTCTGCAAGATAGGATTCATCACCACTTATAGGGAGAGATCTGAAAGTTTAAA
ATTGTACCCAAGGTCACACAGCTGGTAAGTGCCAGAGCTGGGATTCCGTAGGGTGT
TCANAGTGCCTCTCCTGCCGTAGGCTTATCACAAAAAGTCAAAGTTTGGTCATAAT
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TCCCACCTCACTGCTGTTCACCTTCTGTGGCAGGGAGAGTCATCATTTCCATTTCA
GCTTGTGGAATATCTTGTCATTAACATTCTCATGCAAAAGCCATTTTATGGTGCCC
AATGAANATGGTTAAGCTACTGCCCCAAGCCTNTGGAAGCCTTCCTAATTTTGGAC
TTGCACTATGCAAATTGNATAATATTTTCTCTACCCTAAGCCAAATATTTTCTTCA
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Sequence ID 1081

CGCCGCCGCGCCGCCGTCGCTCTCCAACGCCAGCGCCGCCTCTCGCTCGCCGAGCT
CCAGCCGAAGGAGAAGGGGGGTAAGTAAGGAGGTCTCTGTACCATGGCTCGTACAA
AGCAGACTGCCCGCAAATCGACCGGTGGTAAAGCACCCAGGAAGCAACTGGCTACA
AAAGCCGCTCGCAAGAGTGCGCCCTCTACTGGAGGGGTGAAGAAACCTCATCGTTA
CAGGCCTGGTACTGTGGCGCTCCGTGAAATTAGACGTTATCAGAAGTCCACTGAAC
TTCTGATTCGCAAACTTCCCTTCCAGCGTCTGGTGCGAGAAATTGCTCAGGACTTT
AAAACAGATCTGCGCTTCCAGAGCGCANCTATCGGTGCTTTGCAGGAGGCAAGTGA
GGCCTATCTGGTTGGCCTTTTTGAAGACACCAACCTGTGTGCTATCCATGCCAAAC

GTGTAACAATTATGCCAAAAGACATCCAGCTAGCACGCCGCATACGTGGAGAACGT
GCTTAAGAATCCACTATGATGGGAAACATTTCATTCTC

Sequence ID - 1083 nt: 198
GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACA
TTGGTTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAAACAATTTAAAACAA
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AAAAAAAAAAAAAAAAAAAAANTTTTAACC

Sequence ID - 1084 nt: 198
GCGCGTCGACTTTGTTTAGACATTGAATGACTTTGTTAAAGGCACAATTAATCACA
TTGGTTGTACTCTGNNGACAGCCTTCTTTAAAAAAAAAATAAACAATTTAAAACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAANTTTTAACC

Sequence ID - 1099 nt: 561
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AAGGTCGTGACTGTTTAAATAGACGGCAAGGTGGAACCTTTTGAAAGATGAGCTT
TTGAATATAAGTTGTCTGCTAGATCATGGTTTGTATTGAACTAACAAGGTTTGCAG
ATCTGCTGACTTATATAAAGCTTTTTGATTCCTACTAAGCTTTAAGATTTAAAAAA
TGTTCAATGTTGAAATTTCTGTGGGGCTCTATTTTTGCTTTGGCTTTCTGGTGAGA
GAGTGAGGAAGCATTCTTTCCTTCACTAAGTTTGTCTTTCTTGTCTTCTGGATAGA
TTGATTTTAAGAGACTAAGGGAATTTACAAACTAAAGATTTTAGTCATCTGGTGGA
AAAGGAGACTTTAAGATTGTTTAGGGCTGGGCGGGGTGACTCACATCTGTAATCCC
AGCACTTTGGGAGGCCAAGGCAGGCAGAACACTTGAAGGAGTTCAAGACCAGCGTG
G

Sequence ID 1109
TTTGNCGGTNTTGGANNNNNANAANTTTCTTCCANNCNTNACNTNTTGGTGGNCTA
AATTAANATGGNTTTNGNGGGTTCNTTNCTNNNTNNNNCATGGGANANAATTNATT
NTCNTNCNNNTTCCTTNNCCCTNAANCTACCTTCCCCCNATTTTCTCCCCTNTTCN
TNAATTANCATCCTCTCCNCNTANNTCNANACNTTAATGGCAANACTATCTAATAN
CNANNATAANANCTCCTGTNNNCCACATNTCTTATTNNNCGCNNCANGTTNCANNC
CCNCAGAGTNAACTCATCCTCNNCNNAANTTCATATCGTGNNCTNTNNNCNNTNGC
GCGANATATTAANNANACCNGTANNTNNNANACANNANNTNNGNAANAANCCTTCT
NANNTTTTAGCNTCNNGCNNTAACNNNNNTCTTNGTGNNNNCNCAGCTTTCNCNNC

ATNATNCTNCNNCGAANTNTCANNCNTCTCCNCTTNAATGNNTTCCCATGNATTAA NTNCCTCGNNNANAGCACTATCGTNNNNGAGNNNATTATNGNCNNTTTACNTCATG TGGTCCANTNNCGTTNGNCGCNNNNAATNTTCGTNNNNCNN

Sequence ID 1118
GGATTTTAGAGGAAGGCGCTNGGTTACATTGGAGAACTGGAGTGGTCTGGAGTTCC ACGGTGTAGTGGACCAGAGGCCACCTCTCCTGGGCTTCTCAGTGTCTCGCCGGCGG GGTTCGGCCTGAGCTGGATTGACATAGCCCTTGGCGGATTTAAACAACCTAAACAT TAAGCAGTACAGCTGCCTCAAACCTTTGGGATTTTCAGAATGACTGACACTGCCGA AGCTGTTCCAAAGTTTGAAGAGATGTTTGCTAGTAGATTCACAGAAAATGACAAGG AGTATCAGGAATACCTGAAACGCCCTCCTGAGTCTCCTCCAATTGTTGAGGAATGG AATAGCANAGCTGGTGGGAACCAAAGAAACAGAGGCAATCGGTTGCAAGACAACAG ACAGTTCAGAGGCAGGGACAACAGATGGGGGTGGCCAAGTGACAATCGATCCAATC AGTGGCATGGACGATCCTGGGGTAACAACTACCCGCAACACAGACAAGAACCTTAC TATCCCCAGCAATATGGACATTATGGTTACAACCAGCGGCCTCCTTACGGTTACTA CTGATAGAAATGTTGGCAGCTTTTAGTAAAAGCATTTACTCTGTTACCATGAGAAA

Sequence ID 1125
NGACTGGCTCCCGAAAAGAAGGGTGGCGAGAANAAAAAGGGCCGTTCTGCCATGGA CGAAGTGGTAACCCGCGAATACACCATCAACATTNACAAGCGCATCCATGGAGTGG GCTTCAAGAANCGTGCACCTCGGGCACTCAAAGAGATTCGGAAATTTGCCATGAAG GAGATGGGAACTCCATATGTGCGCATTGACACCAGGCTCAACAAANCTGTCTGGGC CAAAGGAATAAGGAATGTGCCATACCGAATCCGTGTGCGGCTGTCCANAAAACGTA ATGAGGATGAAGATTCACCAAATAAGCTNTATACTTTGGTTACCTATGTACCTGTT ACCACTTTCAAAAATCTACAGACAGTCAATGTGGATGANAACNAATCGCTGATCGT CAGATCAAANAAANT

Sequence ID - 1139 nt: 503
CAGCACTGCCAGTGGAGATGGGCGTCACTACTGCTACCCTCATTTCACCTGCGCTG TGGACACTGAGAACATCCGCCGTGTGTTCAACGACTGCCGTGACATCATTCAGCGC ATGCACCTTCGTCAGTACGAGCTGCTCTAAGAAGGGAACCCCCAAATTTAATTAAA GCCTTAAGCACAATTAATTAAAAGTGAAACGTAATTGTACAAGCAGTTAATCACCC ACCATAGGGCATGATTAACAAAGCAACCTTTCCCTTCCCCCGAGTGATTTTGCGAA ACCCCCTTTTCCCTTCAGCTTGCTTAGATGTTCCAAATTTAGAAAGCTTAAGGCGG CCTACAGAAAAAGGAAAAAAGGCCACAAAAGTTCCCTCTCACTTTCAGTAAAAATA AATAAAACAGCAGCAGCAAACAAATAAAATGAAATAAAAGAAACAAATGAAATAAA TATTGTGTTGTGCAGCATTAAAAAAAATCAAAATAAAAATTAAATGTGAGCAAAG

Sequence ID - 1148 nt: 587

TGAAAAATAAAGTTTTTATGTATATTCTACATATGTATATGTTGGTAGAAAGCAAA
AACGCTAGGTAAAAATAAATGTAATACAATTTTAGCTATGAACCAAAAAACCATTT
GTGGTGTGGATGCAAGAAAGTCTGGATGGGTGCAGAGTTCTCCATGTTTCACTTCT
GACATTTGAAAATACGCAGTTTGCATTTGATACGTCAAATGTTATTTTTAAGAAAA
CCAATAAAATCATTAAAACCGAAAAGGCAGTTTTGCTTGTTTTTACCTTAGTTGGA
GTTATCTGCAATTGCCGTATTAGTGTTTTAAGGAACTTGTAAGTAAGCTCCTTAGT
CCCCTTTAGAGCTACGAAACATGTCAATTTTACTTTTCTCCAGCTTTTTGGAATCT
TATCTAAATTACCATGTAGAGTTCTGCATAGCTTCAAATTCTCTTAGCCAATGTGG
TCTGTAAGTGTCTATCGATGAATTTCACCGTTAATTGCCGTAGTATACTGTCCTGT
ACCGGATGTGAAGAGGAGCAACTCTGCACAGTGCACTGGTTGCTCCCATGGTAGGA
ANGAATGGCTTATCAATGGTCGGATTT

Sequence ID - 1160 nt: 650

GGAGGATGGAGCAGTGAGCGGGTCTGGGCGGCTGCTGGCAGCGCCATGGAGACGGT
ACAGCTGAGGAACCCGCCGCGCCGGCAGCTGAAAAAGTTGGATGAAGATAGTTTAA
CCAAACAACCAGAAGAAGTATTTGATGTCTTAGAGAAACTTGGAGAAGGGTGAGTG
TAAAGAAACTATAGGTAGGTCATTGGGTCCCAGTCTTTTTCCTGCCCCAGAAGAAG
CAGAAGGATATGAACCTTTCAGCATTGTTCTAGGTGGGGTGGAAGGTAAATTTACA
GCTTGTGATGTCCTTCTTCGCTTTACTCCAATCCCTATTATAGACAGATTTAGTGA
TTCCTGGTCTTTTTAACACGAAGAATATCTATTGTTTTCTCTTTTGTAGGATCTGT
ATGATTTTATCTACTTAACAGATAGCACTAATTAGATTAAAATTCTATAAGAAACT
TTTTAATTTGCTGTTCATAATTTCTGATTGGTATGCAATAACTGTTTCAATGAAAA
TCAATGTAATTTAGTATTTTAATATTTGCACCTTTGTGAAATATAGTAAATAAATT
AAGCACTATCACCACCTTCACAGCTACTTAGGAGATCCACAATCCTGGGTTGGGAG
CCAGTGGATTTCCTGAAACACAGATTTGTTAATG

Sequence ID - 1165 nt: 502

CTCAAGTGAATCCTGGCTTCTTGGAAGCGCTTGCCTAGACGAGACACAGTGCATAA
AAACAACTTTTGGGGGACAGGTATGTTTTCTTGCAGCTGCGGTTGTAAGGTCTTGG
CAAGACAAGCAGTGTGGCCAGAATTTTGAACTTCTGATGAATGTGTAATGCAAAGG
ACCTTGTACATTTTTTTGTTTCAAGGTCCTCAAAATGAGCACATGAAGAGGTTGCT
GTGAAACTTTAAGTGGCCCTACTGCGCAGAAGCATTCAGATGTCACTTGATGATCT
GTAAGGGAACTTGCTGATTTGGGAATGTGCTTAGGGAACACACATTCCTTTTGACA
GGGTCTGTCACTGGGTGGGTGATGAATTATACAGATGACATGTGCTTTTTTTTCTT
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Sequence ID - 1172 nt: 648

CCACAATAATAAGAGAAAAACAGGAGCAAAAGGATATACAAAACCACCAGAAAACA
AATAACAAAGTGACAGGAGTAAGTCCTTAACTGGCAATAATAACCATGAATCTAAA
TGGATTCCATTTCCCACTTAAAAGATAAAGACATGCTGAATGGATAAAAAGCTGTC
ACCCAGTTATATGCTGCCTACAACAAACTCACTTCACCTGTAAACATACATATGGA
TGGAAAGAGAAGGCATGGGAAAAGATACTCTACTCAAATGAAAACAAAAACCAAAC
AAAGGTGGCTATTCTTATATGAGATAATACAGACATTAAATCAAAAACTGGAAACA
AACACAAAGTCATTGTATAATGATGAATTCAATTATATCATGATGAATTCAATTAT
ATCCTCCTTCCTGATCAATTCAGAAAGGAGGATATAATCTTTTTAAATATATATAC
ACCCAACACCAGAGCATATAAATATGTAAAGGAAGATAAAGGGAGTCCTGTGATCA
AGAATAAATATAACAATTATAAATATTTTATCTAAAGTGATAGATAGACTGTAATA
CAATAATAGGGTGGTGACATTAACACCCCCTCTCACATTGGACTGATCATCTAGAA
GGGAGAAAAAGCTTTATGATTGGAAAAGCCAT

Sequence ID 1178

ATTGTGTTGGCCACCCGGGAATTCGCGGCCGCGTCGACCTACGCACACGAGAACAT
GCCTCTCGCAAAGGATCTCCTTCATCCCTCTCCAGAAGAGGAGAAGAGGAAACACA
AGAAGAAACGCCTGGTGCAGAGCCCCAATTCCTACTTCATGGATGTGAAATGCCCA
GGTGAGGAGACGGCTTGCTGTAGTGGGGAAAGCACTGGACCTCAACAGTTGGAAAA
TGTTGTAGTGTTAGCTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTTCAGTTTCTT
CGCCTGTGGAAAATATTTTCCCTGATACTCTTAAAATTTGAATGTATGAGACTGGC
AAAGTTTTGCATCTTAGGAGGAGTGATTCATTTCACCGTGATCTCTCATCACATTT
CACATACAACCCCTACGTTTTTTTGTGTTGGGAAACAATGTAATGGATGATGAGTT
GGGCATAAGTGCAGGAAAGACGGGTGTAATAGAGGAAAAAAATGTTATCTGCTTTT
CTTTCAGGATGCTATAAAATCACCACGGTCTTTAGCCATGCACAAACGGTAGTTTT
GTGTGTTGGCTGCTCCACTGTCCTCTGCCAGCCTACAGGAGGAAAAGCAAGGCTTA
CAGAAGGATGTTCCTTCAGGAGGAAGCAGCACTAAAAGCACTCTGAGTCAANATGA
GTGGGAAACCATCTCAATAAACACATTTTGGAT

Sequence ID - 1180 nt: 622

CTTTTCCTCCCGCTGTCCCCCACGGGAGGGGACTGCTCTCCCCCGCTGCATCCTTT
CTGTGAGGTACCTTACCCACCTCAGCACCTGAGAGGGTGAAATAGAATTCTAACCT
CGACATTCGGGAAGTGTTTTTGAGAAGTCTCGGTCGGTAAGGGAAGTCTTCCAAGT
CCGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAG
GCAGCTGTGACTGTGTCAAGGGAAGCCACGACTCTGACCATAGTCTTCTCTCAGCT
TCCACTGCCGTCTCCACAGGAAACCCAGAAGTTCTGTGAACAAGTCCATGCTGCCA
TCAAGGCATTTATTGCAGTGTACTATTTGCTTCCAAAGGATCAGGCCCTGAGAACA

ATGACCTTATTTCCTACAACAGTGTCTGGGTTGCGTGCCAGCAGATGCCTCAGATA
CCAAGAGATAACAAAGCTGCAGCTCTTTTGATGCTGACCAAGAATGTGGATTTTGT
GAAGGATGCACATGAAGAAATGGAGCAGGCTGTGGAAGAATGTGACCCTTACTCTG
GCCTCTTGAATGATACTGAGGAGAACAACTCTGACANCCACAATCATGAGGATGAT
GTGTTG

Sequence ID - 1181 nt: 155
CGCCACTTATCCAGTGAACCACTATCACGAAAAAAACTCTACCTCTCTATACTAAT
CTCCCTACAAATCTCCTTAATTATAACATTCACAGCCACAGAACTAATCATATTAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Sequence ID 1182
CATTGTGTTGGCNCCCGGGAATTCGCGGCCGCGTCGACTTTTTGTGTTGTTTGGAG
CAGAAATACTAAAGAAGATTCCGGGCCGAGTATCCACAGAAGTGGACGCAAGGCTC
TCCTTTGATAAAGATGCGATGGTGGCCAGAGCCAGGCGGCTCATCGAGCTCTACAA
GGAAGCTGGGATCAGCAAGGACCGAATTCTTATAAAGCTGTCATCAACCTGGGAAG
GAATTCAGGCTGGAAAGGAGCTCGAGGAGCAGCACGGCATCCACTGCAACATGACG
TTACTCTTCTCCTTCGCCCAGGCTGTGGCCTGTGCCGAGGCGGGTGTGACCCTCAT
CTCCCCATTTGTTGGGCGCATCCTTGATTGGCATGTGGCAAACACCGACAAGAAAT
CCTATGAGCCCCTGGAAGACCCTGGGGTAAAGAGTGTCACTAAAATCTACAACTAC
TACAAGAAGTTTAGCTACAAAACCATTGTCATGGGCGCCTCCTTCCGCAACACGGG
CGAGATCAAAGCACTGGCCGGCTGTGACTTCCTCACCATCTCACCCAAGCTCCTGG
GAGAGCTGCTGCAGGACAACGCCAAGCTGGTGCCTGTGCTCTCAGCCAAGGCGGCC
CAAGCCAGTGACCTGGAAAAAATCCACCTGGATGAGAAGTCTTTCCGTTGGTTGCA
CAACGAGGACCAGATGGCTGTGGAGAAG

Sequence ID - 1183 nt: 479
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AGATTCAAGGGCCAGATCTTGATGCCCAACATTGGTTATGGAAGCAACAAAAAAAC
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TCCTCCAAGAACCGCAAAGCCATCGTGGAAAGAGCTGCCCAACTGGCCATCAGAGT
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Sequence ID - 1185 nt: 628

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AGAATATACAGAAAAGGGGAGTTGGGTGAAGAATCACCATATTCTCATTACCAGAG
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TTTTTAGATCCTTGTAATACTAGTAAAGATATTCCACTCTGTGTTGTAAGCATTTT
TCCATTTTGCTCCATGGTCTTCATAATGCCCTGTGGTCCTTTATTAAGGGGATGCA
CCATGTAGAGGTGAAAGGCTTTCCTTGACTTGGCCACCATTTCTGTATTTTCCTTA
GAGGAGGAGGTTTCCAACATTTCTTTTTTAGAGACAGAGTCTCGTTCTGACACGCA
GGCAGGAGTGCAGTGGCATGATAACAGCTCACTGCAGCCTCGAACTCCTGGGCTCA
AGTTATCCTCCCACCTCAGCTTCCTGAGTAGCTAGGACTGCAGGTGCCTGCCACCA
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Sequence ID - 1186 nt: 494

CAGCCCTCCGTCACCTCTTCACCGCACCCTCGGACTGCCCCAAGGCCCCCGCCGCC
GCCTCCAGCGCCGCGCAGCCACCGCCGCCGCCGCCGCCTCTCCTTAGTCGCCGCCA
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GCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCTCCTACGTTTACCTGTCCAT
GTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACTTTC
TTCACCAATCTCATGAGGAGAGGGGAACATGCTGAGAAACTGATGAAGCTGCAGAA
CCAACGAGGGTGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACTGTGATGAC
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Sequence ID - 1188 nt: 599

GGGAGACAAGCCCAGCCTTTCGGCGAGNATACGTCTAACCCTGTGCAACAGCCACT
ACATTACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATT
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AACAAGTACTTCTTGATACCTGGGATACTGTGCCCAGAG

Sequence ID 1189

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CATTACTTCAAACTGAGATCCTTCCTTTTGAGGGAGCAAGTCCTTCCCTTTCATTT
TTTCCAGTCTTCCTCCCTGTGTATTCATTCTCATGATTATTATTTAGTGGGGGCG
GGGTGGGAAAGATTACTTTTTCTTTATGTGTTTGACGGGAAACAAAACTAGGTAAA
ATCTACAGTACACCACAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCG
TGGAAAGGGGCAGGCCAGAGCTACCCGCAGAGTTCTCAGAATCATGCTGAGAGAGC
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TAAAGCCCAGAGACAGCTTGATCAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTA
GCTGGAGGGACCTTGTCTCCCAGCTCAGGGCTCTTTCCTCCACACCATTCAGGTCT
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Sequence ID 1190

GTTTAAATTTGACAAACTAAAGCTNATNACTGCTATAAGAGTAATAACTGCTCATT
TTCCATAACTCATTCTTAAAGTTTTAGTAATGTAAAAGTTATTTTTTTGCAGTAAG
TTATAATGATAGAAGCTTACATGTTTTTTCATGCCTCATCTGTTTCCCCTTAAAAC
TATAATTATCAGTAAAGTCCTGTGGTATTTTTCAATTTGTAAGAAACTAGGCTATA
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TGGTAATTGTGTGCTATTGCTTTTTGTTGACTTGCAAAAAAAAAAAAAAAAAAATT
ACTATGACTTGNGGTAGCCCTGCAACCTTCGGAAGTGCTTAGCCCAGTCTGACCAT
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AAGATACTATATAATATCTCATAATTTTAAAAATCACTGTTTTGTATAATAATAAA
ACAAGGCAGGCAAGCTGTTCTACAATGACTGTTGGTAAGGGTGCTGAGGAAGAAAA
ACAAACAATCTTGATTCAGGGATAGTGAATAGACAAAAAATGTCCTAATCAATGAA
GCTGTGTGATGATTCTGATTGACAGAGA

Sequence ID 1191

GTGCAAAGTGTTATATCCACTTTCAACAAAGAGAGAAGCTGAAAAGCTAACCCAAT
GTTAATTTTGGATCACACACATTCAGTGTAGACTTTAAGATTTTACTTCTGTTGGA
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TACTTGTTTAATATTTTTCTCTTCCAATTAGGAACTCAATATGGAATAAAAAATAT
TTAAATGTATTTTACTCAAACGTGTGTGTATATATGTTTGTGTGCATGATAAGGAG
AGTGAGAGCAAGAGTAAGAGAGAGAGAGCACGCATAGATGGAAGCACACATTTAAT
GTCTATGAAATGAGAAAACATTAAGGCTAAGATATTTTTCCTTCTGAACTAGCAGA
TTGTATCAATGGCTGGTCACTTAAATTAATCAGTTTGTAAAGATATTTAAAAGGTA
TGTCTACCTTCTTGCAATTAATTTGATTATGTTCTAATGGCATGGCAAGAGAAATG

AAAGAAGATAACTAAAAGTTAAAAGTCGTTGCATGTTTTTGTTGCAGCATACCCTT
CTTTCAGGCTACCGAATAACCTTGATTGACATTGGATTAGTAGTAGAATACCTCAT
TGGTAGAGCATATCGCAGCANCTACACTAGAAAACAT

Sequence ID 1192
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ATTACAGCTGTGAAGCCACCGCGCCCGGCTGCTGTGATAGTTGAGATGTAAACCAA
AAATAAAATTCTAAGCCACCCAATCCGACTGAATGGACCCTTCCTGTTGAGCAAGG
ACATTCCAAAGTAAACTGAAAAGACCAGCTTAGGCCATGATGGGAAGGGGAGGTGT
CAACATGCCTCATTCTACCTTCCTCCCTCTGGAATCCAGACACAACTGACCAGCAT
TAACATTAAAACAGAGATCTTAAGCTGGGCACGGTGGCTCATGCCTGTAATCCCAG
CACTTTGGGAGGCCAAGGTGGGATCACCTGAGGTCGGAAGTTCAAGACCAGCCTGG
CCGGTATGGTGAAGCCATGTCTCTACTGAAAATGCAAAATTGGCCGGACATTGTGG
TGCA

Sequence ID 1193
TNCNTTTTTTTTCCCNCGGGAAAGCGCGCCATTGTGTTGGTCCCCGGGAATTCGCG
GCCGCGTCGACGAGAAATGGCTTGAACCCAGTAGGCAGAGGTTGTAGTGAGCCCAG
AATNGGNCACCTGCACNTTTANCCNTGGGTGACAAAANTGAAAACTTTGTCTNAAA
AAAAAAAAAAAAAAATTTTAANTNAAATNAAAAANCCTTTNCNTTNTTTTTNAAAN
NGGGGGGGGNNTTTTTNGGGNTTNGNNNTGGTAAAAANTNNNTTTTTTTTTTTTTA
GGGGCCNANNCCCCNTTTTANAAAANCCNGNTTTTNAAAAAANTTTTTNCCCNCN
NTTNGGGGGGGGGGNTTTTNANCNNTNTTNGGGGGGGNNCCCCTNTTANNACCNNC
AAANTTTTTANTTTTTTGNNNAANNNCCCCCTTTTTTNNTTTTTTTTGNGGGGGGG
GGGNNGCCCCCNNCCTTTNGGGGGGGGGGNTTNNGNAAAANNACTTTTNAAAANNA
AGGGNNGGGGGNANATNNCCCCCCCNGGNTTTTTTTTTTAAAAANTNAANNGGGGG
GGGNNNCTNANTNGGGGCNCCCANNGGGGGNTTANAANNATTTCTNCCCAAACCC
CCNGNTTTTATNNCCCCCCCCCCCCNCNNNNGAANGGGNGGNCCNTTTTTTTTATT
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TTTTNGGNAAANCCNNGGGGGGNTCCTTTTTNAAANNNNCCCCCAAAAAAAANTTT
TTTTNTTNTNTTTTTCTCTNGGGGNCCNNANTTNTANANTTTTNCNCCNAAAAAAA
ANGGGNCCCCTTTTTTTNCNGGNNGGNNCCCAAAANNTTTTTTTTNAAAAAAAAAA
AAAA

Sequence ID 1195
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AGAGTGTTAGGCCTGAGCTTGAGAGCCCTGGAGAGACGTGTGCACAAAATGTGACC

TGAGGCCCTAGTCTAGCAAGAGGACATAGCACCCTCATCTGGGAATAGGGAAGGCA
CCTTGCAGAAAATATGAGCAATTTGATATTAACTAACATCTTCAATGTGCCATAGA
CCTTCCCACAAAGACTGTCCAATAATAAGAGATGCTTATCTATTTTA

Sequence ID - 1196 nt: 412
GTCGACGCGGCCGCGGTCGCTGGAGNCGATCAACTCTAGGCTCCAACTCGTTATGA
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AGAGTACTATGCTATGTTGGCTAAAACTGGTGTCCATCACTACAGTGGCAATAATA
TTGAACTGGGCACAGCATGCGGAAAATACTACAGAGTGTGCACACTGGCTATCATT
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TAATAAAATTTGCTTGTTTT

Sequence ID 1197
CCGCCAACATGGGCCGCGTTCGCACCAAAACCGTGAAGAAGGCGGCCCGGGTCATC
ATAGAAAAGTACTACACGCGCCTGGGCAACGACTTCCACACGAACAAGCGCGTGTG
CGAGGAGATCGCCATTATCCCCAGCAAAAAGCTCCGCAACAAGATAGCAGGTTATG
TCACGCATCTGATGAAGCGAATTCAGAGAGGCCCAGTAAGAGGTATCTCCATCAAG
CTGCAGGAGGAGGAGAGAGAAAGGAGAGACAATTATGTTCCTGAGGTCTCAGCCTT
GGATCAGGAGATTATTGAAGTAGATCCTGACACTAAGGAAATGCTGAAGCTTTTGG
ACTTCGGCAGTCTGTCCAACCTTCAGGTCACTCAGCCTACAGTTGGGATGAATTTC
AAAACGCCTCGGGGACCTGTTTGAATTTTTCTGTAGTGCTGTATTATTTTCAATA
AATCTGGGACAA

Sequence ID 1198
CAGAGGTGGGAGGATTGCTTCAGTTCAAGAGTTTGAGACCAGCCTGGGTAACATGG
CGAAACCCTGTCTTTACAAAAAATGCAAACCTTTGCCGCATGTGTTGGGGTGCGCC
TGTAGTCCCAGCTTCTCGGGAGGCTGAGGTGGGGGGACCACCTGAGCCATGGAGGT
TGAGGCTGCAGTGAGCCGTGATACCACCACTGTACTCTAGCCTGGGCCATAGAGTG
AGACACCCTGCCTCAGAAATA

Sequence ID - 1199 nt: 439
CCCATCCCCTCGACCGCTCGCGTCGCATTTGGCCGCCTCCCTACCGCTCCAAGCCC
AGCCCTCAGCCATGGCATGCCCCCTGGATCAGGCCATTGGCCTCCTCGTGGCCATC
TTCCACAAGTACTCCGGCAGGGAGGGTGACAAGCACACCCTGAGCAAGAAGGAGCT
GAAGGAGCTGATCCAGAAGGAGCTCACCATTGGCTCGAAGCTGCAGGATGCTGAAA

TTGCAAGGCTGATGGAAGACTTGGACCGGAACAAGGACCAGGAGGTGAACTTCCAG
GAGTATGTCACCTTCCTGGGGGCCTTGGCTTTGATCTACAATGAAGCCCTCAAGGG
CTGAAAATAAATAGGGAAGATGGAGACACCCTCTGGGGGTCCTCTCTGAGTCAAAT
CCAGTGGTGGGTAATTGTACAATAAATTTTTTTTTGGTCAAATTTAA

Sequence ID - 1200 nt: 526

CTGGAGACGACGTGCAGAAATGGCACCTCGAAAGGGGAAGGAAAAGAAGGAAGAAC
AGGTCATCAGCCTCGGACCTCAGGTGGCTGAAGGAGAGAATGTATTTGGTGTCTGC
CATATCTTTGCATCCTTCAATGACACTTTTGTCCATGTCACTGATCTTTCTGGCAA
GGAAACCATCTGCCGTGTGACTGGTGGGATGAAGGTAAAGGCAGACCGAGATGAAT
CCTCACCATATGCTGCTATGTTGGCTGCCCAGGATGTGGCCCAGAGGTGCAAGGAG
CTGGGTATCACCGCCCTACACATCAAACTCCGGGCCACAGGAGGAAATAGGACCAA
GACCCCTGGACCTGGGGCCCAGTCGGCCCTCANAGCCCTTGCCCGCTCGGGTATGA
AGATCGGGCGGATTGAGGATGTCACCCCCATCCCCTCTGACAGCACTCGCAGGAAG
GGGGGTCGCCGTGGTCGCCGTCTGTGAACAAGATTCCTCAAAATATTTTCTGTTAA
TAAATTGCCTTCATGTAAACTG

Sequence ID - 1201 nt: 613

CTTAAGTATGCCCTGACAGGAGNATGAAGTAAAGAAGATTTGCATGCAGCGGTTCA
TTAAAATCGATGGCAAGGTCCGAACTGATATAACCTACCCTGCTGGATTCATGGAT
GTCATCAGCATTGACAAGACGGGAGAGAATTTCCGTCTGATCTATGACACCAAGGG
TCGCTTTGCTGTACATCGTATTACACCTGAGGAGGCCAAGTACAAGTTGTGCAAAG
TGAGAAAGATCTTTGTGGGCACAAAAGGAATCCCTCATCTGGTGACTCATGATGCC
CGCACCATCCGCTACCCCGATCCCCTCATCAAGGTGAATGATACCATTCAGATTGA
TTTAGAGACTGGCAAGATTACTGATTTCATCAAGTTCGACACTGGTAACCTGTGTA
TGGTGACTGGAGGTGCTAACCTAGGAAGAATTGGTGTGATCACCAACAGAGAGAGG
CACCCTGGATCTTTTGACGTGGTTCACGTGAAAGATGCCAATGGCAACAGCTTTGC
CACTCGACTTTCCAACATTTTTGTTATTGGCAAGGGCAACAAACCATGGATTTCTC
TTCCCCGAGGAAAGGGTATCCGCCTCACCATTGCTGAAGAGAGAGACAAAAGA

Sequence ID 1202

GGAATTCGCGGCCGCGTCGACCTCTGCTCGAATTGACAGAAAAGGATTCTGTGAAG
AGTGATGAGATTTCCATCCATGCTGACTTTGAGAATACATGTTCCCGAATTGTGGT
CCCCAAAGCTGCCATTGTGGCCCGCCACACTTACCTTGCCAATGGCCAGACCAAGG
TGCTGACTCAGAAGTTGTCATCAGTCAGAGGCAATCATATTATCTCAGGGACATGC
GCATCATGGCGTGGCAAGAGCCTTCGGGTTCAGAAGATCAGGCCTTCTATCCTGGG
CTGCAACATCCTTCGAGTTGAATATTCCTTACTGATCTATGTTAGCGTTCCTGGAT

CCAAGAAGGTCATCCTTGACCTGCCCCTGGTAATTGGCAGCAGATCAGGTCTAAGC
AGCAGAACATCCAGCATGGCCAGCCGAACCAGCTCTGAGATGAGTTGGGTAGATCT
GAACATCCCTGATACCCCAGAAGCTCCTCCCTGCTATATGGATGTCATTCCTGAAG
ATCACCGATTGGAGAGCCCAACCACTCCTCTGCTAGATGACATGGATGGCTCTCAA
GACAGCCCTATCTTTATGTATGCCCCTGAGTTCAAGTTCATGCCACCACCGACTTA
TACTGAGGTGGATCCCTGCATCCTCAACAACAATGTGCAGTGAGCAT

Sequence ID - 1203 nt: 692
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TTTCACAATGTCCGGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTA
AGTTCCTTGCAGCAGGAACCCACTTAGGTGGCACCAATCTTGACTTCCAGATGGAA
CAGTACATCTATAAAGGAAAAGTGATGGCATCTATATCATAAATCTCAAGAGGAC
CTGGGAGAAGCTTCTGCTGGCAGCTCGTGCAATTGTTGCCATTGAAAACCCTGCTG
ATGTCAGTGTTATATCCTCCAGGAATACTGGCCAGAGGGCTGTGCTGAAGTTTGCT
GCTGCCACTGGAGCCACTCCAATTGCTGGCCGCTTCACTCCTGGAACCTTCACTAA
CCAGATCCAGGCAGCCTTCCGGGAGCCACGGCTTCTTGTGGTTACTGACCCCAGGG
CTGACCACCAGCCTCTCACGGAGGCATCTTATGTTAACCTACCTACCATTGCGCTG
TGTAACACAGATTCTCCTCTGCGCTATGTGGACATTGCCATCCCATGCAACAACAA
GGGAGCTCACTCAGTGGGTTTAATGTGGTGGATGCTGGCTCGGGAAGTTCTGCGCA
TGCGTGGCACCATTTCCCGTGAACACCCATGGGAGGTCATGCCTGATCTGTACTTC
TACAGAGATCCTGAAGAGAT

Sequence ID 1204
TTTTTTTTTTTTTCCTGCGGGAAAGCGCGCCATTGTGTTGGTACCCGGGAAATTCG
CGGCCGCGTCGACACAGGCCCCAGCATCAAGATCTGGGATTTAGAGAGGAAAGATC
ATTGTAGATGAACTGAAGCAAGAAGTTATCAGTACCAGCAGCAAGGCAGAACCACC
CCAGTGCACCTCCCTGGCCTGGTCTGCTGATGACACAGGTTGGGCNGGNNCNCNGG
GGNGGNNNNGNNNNGCNGNNGGNNCNGNNNNCNNNNNGCNNNNGNNNNTNNNCNNN
GNNCNNNNNNNNNNNNNNNNNGNTCNNGNNGCNGGGGCCNGGNCGNCGCGGNCGCG
NNTNNNNGGGTNCNNNCNCNNNGGCGCGC

Sequence ID 1205
CAGACTCTGACCCAGCCTCAGTCCTAACTCCTGGGGCTGGGCTGAGGGGAACAAGC
ATTTGCTGAAACTTGAAAAAACAAAGCAAATCAAAAACAGGAAAAAATTGTACCTG
GTACTTTTTTTTAGAAAAAAAGATTAAAAAAGAAAGAATAAATTCTTGTTTGGAAA
CTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAATTTTAAACTC

TNNNNNTNNCNNCNANTAANNCANNTCNANNNNANNNAATTACTTNNANGTNNNTC
ACN

Sequence ID - 1207 nt: 642

ACGAGAAGCCAGATACTAAAGAGAAGAANCCCGAAGCCAAGAAGGTTGATGCTGGT
GGCAAGGTGAAAAAGGGTAACCTCAAAGCTAAAAAGCCCAAGAAGGGGAAGCCCCA
TTGCAGCCGCAACCCTGTCCTTGTCAGAGGAATTGGCAGGTATTCCCGATCTGCCA
TGTATTCCANAAAGGCCATGTACAAGAGGAAGTACTCAGCCGCTAAATCCAAGGTT
GAAAAGAAAAAGAAGGAGAAGGTTCTCGCAACTGTTACAAAACCAGTTGGTGGTGA
CAAGAACGGCGGTACCCGGGTGGTTAAACTTCGCAAAATGCCTAGATATTATCCTA
CTGAAGATGTGCCTCGAAAGCTGTTGAGCCACGGCAAAAAACCCTTCAGTCAGCAC
GTGAGAAAACTGCGAGCCAGCATTACCCCCGGGACCATTCTGATCATCCTCACTGG
ACGCCACAGGGGCAAGAGGGTGGTTTTCCTGAAGCAGCTGGCTAGTGGCTTATTAC
TTGTGACTGGACCTCTGGTCCTCAATCGAGTTCCTCTACGAAGAACACACCAGAAA
TTTGTCATTGCCACTTCAACCAAAATCGATATCAGCAATGTAAAAATCCCAAAACA
TCTTACTGATGCTTACTTCAAAAAGA

Sequence ID 1208

CCCTATACCTTCTGCATAATGAATTANCTAGAAATAACTTTGCAAGGGAGAGCCAA
AGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCTAAAAGAGCACACCC
GTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCGACAAACCTACCGAG
CCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAACTTTAAATTTGCCCA
CAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCAAAGAGGAACAGCTC
TTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATTTAACACCCATAGTA
GGCCTAAAAGCAGCCACCAATTAAGAAAGCGTTCAAGCTCAACACCCACTACCTAA
AAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATCACCC
TATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAG

Sequence ID - 1209 nt: 620

CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAG
GAAGTGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGAT
CCACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACA
CCCTCTTCATGAACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAG
TCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCAC
CGCCAAGTGCCTGAACATCTGGGCCCTGATTTTGGGCATCTTCATGACCATTCTGC
TCGTCATCATCCCAGTGTTGGTCGTCCAGGCCCAGCGATAGATCAGGAGGCATCAT
TGAGGCCAGGAGCTCTGCCCGTGACCTGTATCCCACGTACTCTATCTTCCATTCCT

CGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCCTTGACCTGTATTCCACTTACTCCA
CCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCCTGCATCAGCCCTTTATCCTC
ACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGTTTCTGGTGCTGCTGTG
ACTT

Sequence ID 1210
TTCGTAATTAGAATACTGTTTGGACTTGCTCAACAAGCACCTTATCTTAACAAAAA
GTAACTTATAGAAAAGGGAGACATTCATTTAACTTCAAGCCCATATTATTCTTAAA
AGCTGACTCTTGAAATAGTATTTATTGAGTCATAGTGGAGTCATGGACTTTTTAA
GGGCCGGAAGGGACTATTTAGATCATCCAGTCCCACCCTGTCATTTTATGGAGGAG
GAAACTGAGGCCTAGATAAGATAACCAGTTAGTGGGTCCACTGACCTTTAGGACAG
TAGTCTATCCGTAAGAGACAACATGGAGAAAGAAATACAACGTTTTTATAGTGAAT
TATCATCTTACAAAGAATATTCTTCCCATATCGCACTTTTAAAAAGTGGGTACCTT
AGTCAAATAGGAGAAAAAACCACTTGAGTAGTTTCATCCTCAGGTTTTAGGTGAGG
AAACTGATACTCAGATTAAATAACTTTAAGCACACAGAGCCTGAATGATAGTCTTA
TTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTTTCACTTGCATTT
CCTTTAGTCTTATTTGAGCTCATCTGTGCTTTTAATGTGTACTACGTTAGGTGTTT
TCACTTGCATTTCCTTGTTTGACGTTGACAATAAATCGTGAAGCTGCCTTATCTAA
GGAAGTCCTAAAGTAAATCATTGGAACACA

Sequence ID 1211
CCATTGTGTTGGNACCCGGGAATTCGCGGCCGCGTCGACGGAGTTTTACCTTATTA
CACTTTAATCTCTGGATTTACCCCATCTCATTTCTCTTTTAGGAAAACTGTTTGTA
TGTGGTGGCTTTGATGGTTCTCATGCCATCAGTTGTGTGGAAATGTATGATCCAAC
TAGAAATGAATGGAAGATGATGGGAAATATGACTTCACCAAGGAGCAATGCTGGGA
TTGCAACTGTAGGGAACACCATTTATGCAGTGGGAGGATTCGATGGCAATGAATTT
CTGAATACGGTGGAAGTCTATAACCTTGAGTCAAATGAATGGAGCCCCTATACAAA
GATTTTCCAGTTTTAACAAATTTAAGACCCTCTCAAACTAACAGGCTTAGTGATGT
AATTATGGTTAGCAGAGGTACACTTGTGAATAAAGAGGGTGGGTGGGTATAGATGT
TGCTAACAGCAACACAAAGCTTTTGCATATTGCATACTATTAAACATGCTGTACAT
ACTTTTTGGGTTTATTTGGAAAGGAATGCAAAGATGAAGGTCTGTTTTGTGTACTT
TTAAGACTTTGGTTATTTTACTTTTTGGAAAAGAATAAACCAAGAATTGATTGGGC
ACATCATTTCAAGAAG

Sequence ID - 1212 nt: 374
AGAGCAGCAGCCATGGCCCTACGCTACCCTATGGCCGTGGGCCTCAACAAGGGCCA

CAAAGTGACCAAGAACGTGAGCAAGCCCAGGCACAGCCGACGCCGCGGGCGTCTGA
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TACGAGCGGCGCGCCATGGAGTTACTGAAGGTCTCCAAGGACAAACGGGCCCTCAA
ATTTATCAAGAAAAGGGTGGGGACGCACATCCGCGCCAAGAGGAAGCGGGAGGAGC
TGAGCAACGTACTGGCCGCCATGAGGAAAGCTGCTGCCAAGAAAGACTGAGCCCCT
CCCCTGCCCTCTCCCTGAAATAAAGAACAGCTTGACAG

Sequence ID - 1213 nt: 567
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GTGAGTGCAGAAATCCTGTCAATTCGTCACTTGTGGACAACCTGCAGCTTGCCACA
GCCTACAGTTCCACCACTGTGACCTCTGAAAACCTCCTGAACAAAAGGAAGGAGAC
TTGGAAATCCTGAATGGGCTTGGAGACATTAAGGGAGAACTGCCTCCCTGGACCAA
GGCAGAATTCAATAGAACCAGCAAGAAATTTTCCTATGAATGGGAAAGCAGGTGGC
AGGGGGCAGGGGTGGAAAAGCTTTGTACAGGAATTGTGGAAAAGCTTTTGCATTAT
CTCTAGTCTGAAAGTCACATTTCTCAGTTCCTTTCCACTCTCTTCTGTCAACTTGC
TGTGAGTAAATGACATCTGTCACCTGTGACACGGGCCAGGGACTATCACCATATGG
CCCCCACACATTATCTAGTACCAGCCTGCCTGGGCCATGCCTTTTCCAGTCACTGT
ACCAGCC

Sequence ID - 1214 nt: 620
CTCTCCTGTCAACAGCGGCCAGCCTCCCAACTACGAGAATGCTCAAGGAGGAGCAG
GAAGTGGCTATGCTGGGGGCGCCCCACAACCCTGCTCCCCCGACGTCCACCGTGAT
CCACATCCGCAGCGAGACCTCCGTGCCCGACCATGTCGTCTGGTCCCTGTTCAACA
CCCTCTTCATGAACACCTGCTGCCTGGGCTTCATAGCATTCGCCTACTCCGTGAAG
TCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCCAGGCCTATGCCTCCAC
CGCCAAGTGCCTGAACATCTGGGCCCTGATTTTGGGCATCTTCATGACCATTCTGC
TCGTCATCATCCCAGTGTTGGTCGTCCAGGCCCAGCGATAGATCAGGAGGCATCAT
TGAGGCCAGGAGCTCTGCCCGTGACCTGTATCCCACGTACTCTATCTTCCATTCCT
CGCCCTGCCCCCAGAGGCCAGGAGCTCTGCCCTTGACCTGTATTCCACTTACTCCA
CCTTCCATTCCTCGCCCTGTCCCCACAGCCGAGTCCTGCATCAGCCCTTTATCCTC
ACACGCTTTTCTACAATGGCATTCAATAAAGTGTATATGTTTCTGGTGCTGCTGTG
ACTT

Sequence ID 1215
CACAAGATAGAATGGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAA
GTGACAGTGCCATAGTTTGGACAGTACCTTTCAATGATTAATTTTAATAGCCTGTG

AGTCCAAGTAAATGATCACTTTATTTGCTAGGGAGGGAAGTCCTAGGGTGGTTTCA
GTTTCTCCCAGACATACCTAAATTTTTACATCAATCCTTTTAAAGAAAATCTGTAT
TTCAAAGAATCTTTCTCTGCAGTAAATCTCGCAGGGGAATTTGCACTATTACACTT
GAAAGTTGTTATTGTTAACCTTTTCGGCAGCTTTTAATAGGAAAGTTAAACGTTTT
AAACATGGTAGTACTGGAAATTTTACAAGACTTTTACCTAGCACTTAAATATGTAT
AAATGTACATAAAGACAAACTAGTAAGCATGACCTGGGGAAATGGTCAGACCTTGT
ATTGTGTTTTTGGCCTTGAAAGTAGCAAGTGACCAGAATCTGCCATGGCAACAGGC
TTTAAAAAAGACCCTTAAAAAGACACTGTCTCAACTGTGGTGTTAGCACCAGCCAG
CTCTCTGTACATTTGCTAGCTTGTAGTTTTCTAAGACTGAGTAAACTTCTTATTTT
TAGAAAGTGGAGGTCTGGTTTGTAACTTTCCTTGTACTTAATTGGGTAAAAGT

Sequence ID - 1216 nt: 484

CAACCTTAGCCAAACCATTTACCCAAATAAAGTATAGGCGATAGAAATTGAAACCT
GGCGCAATAGATATAGTACCGCAAGGGAAAGATGAAAAATTATAACCAAGCATAAT
ATAGCAAGGACTAACCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTT
GCAAGGAGAGCCAAAGCTAAGACCCCCGAAACCAGACGAGCTACCTAAGAACAGCT
AAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATAGGTAGAGGCG
ACAAACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAGTTCAAC
TTTAAATTTGCCCACAGAACCCTCTAAATCCCCTTGTAAATTTAACTGTTAGTCCA
AAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAGAGAGAGTAAAAAATT
TAACACCCATAGTAGGCCTAAAAGCAGCCACCAATT

Sequence ID 1217

GACAGGCGGGGGCCCAGCGGCCGGGTGAAGGCCGGGTGGCTCTGTGAATCAAAGGA
GAGTCCCAGAAAACCTGTGACTGTTGAAGAAAATTCATCTGTGAATTTTTATATTC
AAGGAGTCAGTATTTATATTCATCTTTTAAACTGGGAAGATTTATATTTTACTTTA
AAACTTCTTGATAATAATTTACAATGAATGGACACAGTGATGAAGAAAGTGTTAGA
AACAGTAGTGGAGAATCAAGGTAAGTAAGCACTTTGTTATCAATTGTTTACTATGA
AGAGAGTTGAAAACTTGACTTTTTTCTTTATTGTTATTGTTGTTATTTAGTTTTCC
TCATAGGTAGCAGAGTTTTCAGGTTTTCCTCTTAGCTATCCAAATACTAAAAAAAT
TCTGATATACGAACCTTTTTTCATAATACAGGTTTTAATTATATTTTTCATTCAGA
TACACAGTAGATCTTAAATATAGAAAGTTTTTGTTTACTTAAATCTATTTGGAAGT
TTATATTTGAGCTAATAATTAAGCTGGAGCATGTATAATAGATTTAAATTGTTTTG
ACTGTTAGTGAAATTT

Sequence ID 1218

CTCACTTGGTGGGTGAGCCTCCAATGACTACACCCAAGGAGGATTTAACACAGGGA

TTTTATGACTTGCAACAAGTCAGGAGGACATGGGGTTGGGGTAGTTCAGCAGTGCC
TGTCTGAACAAAGGTGAAAATTGGGCTTTTATTGGGCTGATCAAGGGGGAGTAAAG
GCAGCCAGGAGCAGTCGCCTGTCATGCTTCTACCTATATTGCATGTATAGAAAAGG
GAAAATAAACTCCTTCCTGGGCAGGGTTTTAGTATGCTAAGGAGGGGAGTTATTCA
ACTTCAATCCAACTCAAGCATCAGCATTGCTGCGTCCATCCCAGTTTTGTTTTGCT
GGGGCTGAACTTCTTCCTATAACTTTTTGAAACAACAAGAACTCAAGGTGTGACAG
TTACAAGTGGGCCCTTTTTCACAGTGTGTACCTAAACACGTGAGGACCCTGGATTA
CAGAATGACAGACTCGAAGTGACTCAAGTTCCGGTTGTTCATCTTTAGATGGTAAA
GATGGCTGTACGTACTATCCTTGCTTATTTCCAATCTATTGTTTAAACTCTTGTAT
ATGTAATACCGCAGAGGCTAGAGATACAACCTTTGACCAAATGAGTGAATTCAAGT
AATCCATTACTAATGTGATCTGGAAACAAACATGGTGTTGAATGTGCATATGT

Sequence ID - 1219 nt: 559
CTTGGCAGCTCCGTTATGTGCCCAGCTCTTTGCAAGGGCATACTGGGAAATGAGTG
GAGATAAAGGACCCAATCATAAGCATTTTACAGTATGGATACCCCATTTTAAAAAG
GTAAACTGAGGCACAATGCAATTTTTTTTTTTTTTAAGGAGTTTATTTGAGCAAA
CAGTGATTCATGAATCAGGCAGCACCAAACCAGAAGGAGGCTTTGCTGAANAAGGA
TGAGGGACAAGCATTTATAAAGTGAATGTAGATGTAATACAAAGAAAATATTTGAA
CCGGGTGCGGTGGCTTACACTTGTAATCCCAACACTTTGGGAGGCCAAGGCGGGCA
GATCACAAGATCAAGAGATCGAGACCATCCTGGTCAACATGGTGAAACCCCATCTN
TACTAAAAAATACAAAAATTANCTGGGCGTGGTGGTGCGTGCCTGTAGTCCCAGCT
ACTTGGGCGGCTGAGGCAGGANAATTGCTTGAACCCGGGAGGTGGAGGTTGCAGTA
AGCCGAGATTGCACCATTGCACTACTCCAGCCTGGTGACAGAGAGAGACTCCATC

Sequence ID 1220
GANNNGTGCGATANNATGNNTGTCTTTTTTTTAAAGTNTTTCNNATNGNAGNGAAN
CCCCCNNANNTNNCATAANGAGAGATNACTACNGTACANATAGNGNCANACNGATA
GTAGTANCAANATTGTNTTAGCTANATNANTCAATAGATATCNAGATANAANAANA
NCNNGGATATACAGCGATGTNTNANNGGNNNNNNNANGGAACGAACATCNACNTTA
ANNATAAGCTNGNGGAGAGAGACANGTANGTTATANANNAGAATNGNAGTAGGNGT
GATCATAATAGNNNNNANNTANTATATANGATNTTANTGNNCTNTNNTNNGTTTAT
CNNNAATNTCTATNCTNGAGAGNAGCNNNATNNNNAGGCGANGANATTGGGNNNTN
CTCNTNATAGANANCTGGTGTCNNANAANTACNTCATCTATTNANCTCTCACNANA
TGGNANNATANAGNAGNGNNNTNNANAGGANTANGCATAGNGNNTNNCTNAAACAA
AANNNATAAGANNTCTCGNNAANANGGGCCTNTNNTNTAGCGAGGNNTTANTTTNT
ATANTTNTTCNCTCTTNNAATANNTANGATANATGANCTNGNNGTGATANATANNN
NNTACNGTNAANNTNTANTCNTATAATAGATANAAATATAGGATNTTNCTCTGGCN

GGTNGAANANTTNNTNCNNTTTNAATAATGNTGTTAGNGACNGNGNTNTNANANNN
NNTTAGAAAGGTACTCTATATACTNNTATGNTNCGGCNNATAATANAACAGATGTT
TGTATNAATATNAAANAAGGTCNNTTTCGNCAAGAGAANNNTGNCTGGTNATAGAA
TTAGCATAANTTANNTANTATGATNNANTNNTNCTACNANTNTTAGCNNTTNGCAG
NAGTCATTNNGNATNTATNNNGNNTANTAGTNANTTGGGNCTNNTNCAGANTATAT
TNTGNGAANATGAANNTACGNANTCCTNNGNANTATNATNNTGANTANGANAANCN
ANANNTNTTNTANNANTGNCTATANATTGCCNNGATANATTNTNNNAATGAANCGA
TAGCCCGCNCTAAGGANNTNNGTNANNTAAANNTCTCAGATAANNTACNTNTTNNT
TATTAANCNANNATCACANTATANCNGNGACANNNGCGANANTATATGTATGNNAN
TATNACNGNTCCNNNCCGNGAANNTANTCNTANNAGGCATTCNGNNGAGCTNTTCT
NCTAGACNATTTNNANTGAAANNATGCNGNNAAAAACGACNNNCTTNAANTTNTGT
CTACANTCCGCNNTNTTTNTACAGATNGCAGNTAAGNNNANTNANNGCTCTCANCT
NGCTNNNACT

Sequence ID - 1221 nt: 741

AAGCAGAANTNTCTCTAAAAACATTATCTCCTTAAAATCTTGAGGTGCATATNAGA
GCCACAGGCAATCTCTGACATATAAAATTGCAGTACAGGCCTTTCAAATTTGGCAT
TTCACTGGTACAATACAACAACCAAGATATATAATAACTGTACAGTGCCTAGACAT
TCCAGTAAGAACCATTATTTTCTTTAATGTAGAATGATTAATACATATTCTACAAG
GGGCAGTAAGGTTAGTAATTCTATAGGGTATGTCCCGACATAATTTTCAAATTGTA
CAATAACACAAACAACTTTGTTAAGGCCATGTTTTATTTGCTGATTAATGGACAAA
AGGCAATGTAATTTATTTTCAAGTATTTTCTTGAAAGTCTGTGCTCATAAAAATCA
TGAAAAGTTGGAAAGACTGTTAAATCACTGAAACTTCAAATATATCTTACACAATC
TTGTTTGTACAAAAATACAAGTTAAATATAAACATAAAGCAATCATGGTAATTTTA
TGCAAATCTGTTTTATGTGATCATCAGTTATATATAAAAGTTTCTCAGTTCTGTTA
TTTGTGAAAAGATCAATACCAGATTGAATGACTACCTATTGGCAAAGGGCCCTAAA
AAGCTTACTTTAGCACTCATCTTTTACATGGTTAAATGCATTTCCTAATTTGAGAT
CACCTAAACACTGGAAAAGAAAAAAAATGAAAGGGCAGTATGTCCATAAACCAACA
AATAATTTGGCTG

Sequence ID - 1224 nt: 485

CGAAATTTCCTTGTGACACAGAGGAAGGGCAAAGGTCTGAGCCCAGAGTTGACGGA
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AGAGGCCCAGGGTGGGGACTGGGAATTTAAGGAGAGCTGGGAACGGATCCCTTAGG
TTCAGGAAGCTTCTGTGCAAGCTGCGAGGATGGCTTGGGCCGAAGGGTTGCTCTGC
CCGCCGCGCTAGCTGTGAGCTGAGCAAAGCCCTGGGCTCACAGCACCCCAAAAGCC
TGTGGCTTCAGTCCTGCGTCTGCACCACACAATCAAAAGGATCGTTTTGTTTTGTT

TTTAAAGAAAGGTGAGATTGGCTTGGTTCTTCATGAGCACATTTGATATAGCTCTT
TTTCTGTTTTTCCTTGCTCATTTCGTTTTGGGGAAGAAATCTGTACTGTATTGGGA
TTGTAAAGAACATCTCTGCACTCAGACAGTTTACAGA

Sequence ID 1226
GGTTTTTATACTTGCCATGAAACTGTTCTTTGGGATATTATTTTGTTCAGGTTCCC
CACTTGGACAGCAGAGGGGGTGACTCTGCCCATCCCTGCCACTGGTAGCCAGGCGG
GCAATGTCTGCTAGCAGTCTGCTTCTGTCTGAACTCAGCCAGCAGAGGCAAACTCC
CGGTTCCCCGAGAAACACTCTGAAGGCAGGGTGGGTGACTCCACCCACCACCGCCT
CTCCTAGCCATGCAGGCCATGTCTGCTAGAGCTTCCAGCGCAGTGGTCCTAATTCT
GTCTGAATCCGGCTGAGGGGTGCAGCCTCCTGTTACTGCCCAGGGAAACACCCAGA
TGGCAGGGTGGGTGACTCCAACCACCTCTGCCTGTGGTAGCCAGATGGGCCACACC
TGCTAGAGCTTCCAGCCCAGCAGTCCCGCTACTCTGTGGGTGGGTGCCATCCCCTG
TTCCTCTGGGAAGCACCCAGACAGCTGATTACGTGACCCCACCCACTTCTGCAGAT
CCTAGCTGAGCAGGACTTGCTGGTTTGGACAATGCCCAAGCAGGGAAGAGCCCTCA
TTCTCTTATCACTGACAGAGGTGAGATGTCCGANTTTGTANGCTGGTGGAGGAGTG
AGGTGGAGGAGGTATGCCTCT

Sequence ID 1228
GTTATTCAGGTATCCATCAAAATTTTATAAGAGGGCCGGAAACATCGGCTCACACC
TGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGTTCACTTGAGGTCAGGAGTT
CGAGACCAGCCTGGCCAACATGGCAAAACCCCGTCACTATTAAAAATACAAAACAT
TAGCTGGGTGTAGTGGCAGGTGCCTGTAATCCCAGCTATTCGGGAGGCCTAGGAAG
GAAAATGGCTTGAACCTGGGGGTGGAGGTTGGAGTGAGGCAAGATCACACCACTGC
ACTCCAGCCTGGGCGACAGAGCGAGACTCCATCTCAAAAGAAGAAAAAAAAAACAA
CAAAAAAACCTTTATCAGATTATCAGAGGTTATCACTACAGAGGGAGGTAAAATTG
GAGGGAAAAGGTACAAATTTATTTCAC

Sequence ID - 1230 nt: 741
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Sequence ID - 1231 nt: 203
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Sequence ID 1239
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Sequence ID 1255
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Sequence 1256

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NT

Sequence ID 1331

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Sequence ID 1332
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Sequence ID 1335
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TTAAATGTTAATGTTTGTTACATTGTTCAAGAAATAAGTAGAAATATATTCCTTTG
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Sequence ID 1336
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CGTGCAGCACTAACGTATTGGCACCTGCCTCCTCTTCGGCCACCCCCCAGATGAGG
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Sequence ID 1337
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Sequence ID 1338
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AGGGCTGAAACACAGATTTTGTAGGGAGCGTAGGGGAGACTGANAAGACAGGTTCA
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Sequence ID 1344

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Sequence ID 1348

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Sequence ID 1351

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TCAGCACAGCGTGACTGCCTATCAGTGACAATATAAGTGAGCTCTATTTGGATCCC
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Sequence ID 1352

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Sequence ID 1353
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Sequence ID 1355
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Sequence ID 1359
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CACCAAGGCAGTGCATGCATGTTGGGGTTTCCTTTACCTTTTCTATAAGTTGTACC
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TACC

Sequence ID 1360

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Sequence ID 1361

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AACCAAAATTTAAATTGACCTCTGTCCTAGAGTATGAGAGCCACACTGAACAGAAA
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CAATTTAGAGCAAGACAGAGAGAAGTTACATTCAGAGAGGAAAATGCAGTAGTCTA
ACTG

Sequence ID 1364
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Sequence ID 1365
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Sequence ID 1366
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Sequence ID 1367
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Sequence ID 1368

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Sequence ID 1369

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Sequence ID 1370

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Sequence ID 1371
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Sequence ID 1372
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Sequence ID 1374
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Sequence ID 1378
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Sequence ID 1380
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Sequence ID 1382
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Sequence ID 1387
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Sequence ID 1389
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Sequence ID 1390
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Sequence ID 1391

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Sequence ID 1392

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Sequence ID 1394

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Sequence ID 1395

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Sequence ID 1396

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Sequence ID 1397

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Sequence ID 1399
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Sequence ID 1440
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Sequence ID 1447
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Sequence ID 1448
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Sequence ID 1449

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Sequence ID 1450
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Sequence ID 1453
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ACA

Sequence ID 1454
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Sequence ID 1456

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ACCCTGAAAATTTGAGGCAGGTCTCAGTTAAATTAGAAAGTTGATTTTGCCAAGTT
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GAGACCCTGTCT

Sequence ID 1460
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Sequence ID 1490

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AGACCCTGGTGAAGAATTGCATCGTGCTCATCGACAGCACACCGTACCGACAGTGG
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ATGAAAGGAAAAAGAATGCCAAAATCAGCAGTCTCCTGGAGGAGCAGTTCCAGCAG
GGCAAGCTTCTTGCGTGCATCGCTTCAAGGCCGGGACAGTGTGGCCGAGCAGATGG
CTATGTGCTAGAGGGCAAAGAGTTGGAGTTCTATCTTAGGAAAATCAAGGCCCGCA
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TTGTT

Sequence ID 1491

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TTCTGAGCTTACAGTTATTGTGAAATCATTTTAATTATAAATTAAGTGGAGATTTA
CTTAAAATCATGTGTAGAAGTAGCCTGTGATATAGTCCTAGATACATACATTATCA
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GGTAAGAGGTTGTTCTTTT

Sequence ID 1493
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TAGCGGCTATTGATCTGAAATATCCCATAATCAGTGCTTCTGTCTCCAGCATTGTA
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Sequence ID 1494
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Sequence ID 1495

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Sequence ID G6

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Sequence ID - 490 nt: 382

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Claims:

1. A set of oligonucleotide probes, wherein said set comprises at least 10 oligonucleotides selected from: an oligonucleotide as described in Table 1 or derived from a sequence described in Table 1, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

2. A set of oligonucleotide probes as claimed in claim 1 wherein said oligonucleotide probes are selected from: an oligonucleotide as described in Table 2 or derived from a sequence described in Table 2, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

3. A set of oligonucleotide probes as claimed in claim 1 wherein said oligonucleotide probes are selected from: an oligonucleotide as described in Table 4 or derived from a sequence described in Table 4, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide.

4. A set of oligonucleotide probes as claimed in any one of claims 1 to 3, wherein each probe in said set binds to a different transcript.

5. A set as claimed in any one of claims 1 to 4 consisting of from 10 to 500 oligonucleotide probes.

6. An oligonucleotide probe wherein said probe is selected from the oligonucleotides listed in Table 1, or derived from a sequence described in Table 1, or a complementary sequence thereof.

7. A set of oligonucleotide probes as claimed in any one of claims 1 to 5, or an oligonucleotide probe as

claimed in claim 6, wherein each of said oligonucleotide probes is from 15 to 200 bases in length.

8. A set of oligonucleotide probes as claimed in any one of claims 1 to 5 or 7 or an oligonucleotide probe as claimed in claim 6 or 7, wherein the transcript to which said probe binds is derived from a gene which is constitutively moderately or highly expressed.

9. A set of oligonucleotide probes as claimed in any one of claims 1 to 5, 7 or 8 or an oligonucleotide probe as claimed in any one of claims 6 to 8, wherein said probes are immobilized on one or more solid supports.

10. A set of oligonucleotide probes or an oligonucleotide probe as claimed in claim 9, wherein said solid support is a sheet, filter, membrane, plate or biochip.

11. A polypeptide encoded by the mRNA sequence to which an oligonucleotide as defined in claim 6 binds.

12. An antibody to a polypeptide as defined in claim 11.

13. A kit comprising a set of oligonucleotide probes immobilized on one or more solid supports as defined in claim 9 or 10.

14. A kit as claimed in claim 13 wherein said probes are immobilized on a single solid support and each unique probe is attached to different region of said solid support.

15. A kit as claimed in claim 13 or 14 further comprising standardizing materials.

16. The use of a set of probes as described in any one of claims 1 to 5 or 7 to 10 or a kit as described in any one of claims 13 to 15 to determine the gene expression pattern of a cell which pattern reflects the level of gene expression of genes to which said oligonucleotide probes bind, comprising at least the steps of:

a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

17. A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in the sample with the disease, condition or stage thereof.

18. A method of preparing a test gene transcript pattern comprising at least the steps of:

a) isolating mRNA from the cells of a sample of

said test organism, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 specific for a disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in said test sample.

19. A method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

a) isolating mRNA from the cells of a sample of said organism, which may optionally be reverse transcribed to cDNA;

b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides or a kit as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation;

c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind in said sample; and

d) comparing said pattern to a standard diagnostic pattern prepared as described in claim 17 using a sample from an organism corresponding to the organism and sample under investigation to determine the degree of correlation indicative of the presence of said

disease or condition or a stage thereof in the organism under investigation.

20. A method as claimed in any one of claims 17 to 19 wherein said mRNA or cDNA is amplified prior to step b).

21. A method as claimed in any one of claims 17 to 20 wherein the oligonucleotides and/or the mRNA or cDNA are labelled.

22. A method as claimed in any one of claims 17 to 21 wherein said probes are as defined in claim 3 and said disease is Alzheimer's disease.

23. A method as claimed in any one of claims 17 to 21 wherein said probes are as defined in claim 2 and said disease is breast cancer.

24. A method as defined in any one of claims 17 to 23, wherein said set of oligonucleotides as defined in any one of claims 1 to 5, 7 to 10 or 13 to 15 are replaced with a set of oligonucleotides which are randomly selected, preferably from a cDNA library.

25. A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

a) releasing target polypeptides from a sample of one or more organisms having the disease or condition or stage thereof;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said

target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides, in the sample with the disease, condition or stage thereof.

26. A method of preparing a test gene transcript pattern comprising at least the steps of:

a) releasing target polypeptides from a sample of said test organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof) encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides, in said test sample.

27. A method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism comprising the steps of:

a) releasing target polypeptides from a sample of said organism;

b) contacting said target polypeptides with one or more binding partners, wherein each binding partner is specific to a marker polypeptide (or a fragment thereof)

encoded by the gene to which an oligonucleotide of Table 1 (or derived from a sequence described in Table 1) binds, to allow binding of said binding partners to said target polypeptides, wherein said marker polypeptides are specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and

c) assessing the target polypeptide binding to said binding partners to produce a characteristic pattern reflecting the level of gene expression of genes which express said marker polypeptides in said sample; and

d) comparing said pattern to a standard diagnostic pattern prepared as described in claim 25 using a sample from an organism corresponding to the organism and sample under investigation to determine the degree of correlation indicative of the presence of said disease or condition or a stage thereof in the organism under investigation.

28. A method as claimed in any one of claims 17 to 27 wherein said pattern is expressed as an array of numbers relating to the expression level associated with each probe.

29. A method as claimed in any one of claims 17 to 28 wherein said organism is a eukaryotic organism, preferably a mammal.

30. A method as claimed in claim 29 wherein said organism is a human.

31. A method as claimed in any one of claims 17 to 30 wherein the data making up said pattern is mathematically projected onto a classification model.

32. A method as claimed in any one of claims 17 to 31 wherein said disease is cancer or a degenerative brain

disorder.

33. A method as claimed in any one of claims 17 to 32 wherein said sample is tissue, body fluid or body waste.

34. A method as claimed in any one of claims 17 to 33 wherein said sample is peripheral blood.

35. A method as claimed in any one of claims 17 to 34 wherein the cells in the sample are not disease cells, have not been in contact with such cells and do not originate from the site of the disease or condition.

36. A method as claimed in any one of claims 19 to 35 for the diagnosis, identification or monitoring of two or more diseases, conditions or stages thereof in an organism, wherein said pattern produced in step c) is compared to at least two standard diagnostic patterns prepared as described in claim 17 or 25, wherein each standard diagnostic pattern is a pattern generated for a different disease or condition or stage thereof.

37. A method of identifying probes useful for diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

a) immobilizing a set of oligonucleotide probes, preferably as described hereinbefore, on a solid support;
b) isolating mRNA from a sample of a normal organism (normal sample), which may optionally be reverse transcribed to cDNA;
c) isolating mRNA from a sample from an organism, corresponding to the sample and organism of step (b), which is known to have said disease or condition or a stage thereof (diseased sample), which may optionally be reverse

transcribed to cDNA;

d) hybridizing the mRNA or cDNA of steps (b) and (c) to said set of immobilized oligonucleotide probes of step (a); and

e) assessing the amount of mRNA or cDNA hybridizing to each of said oligonucleotide probes to determine the level of gene expression of genes to which said oligonucleotide probes bind in said normal and diseased samples to generate a gene expression data set for each sample;

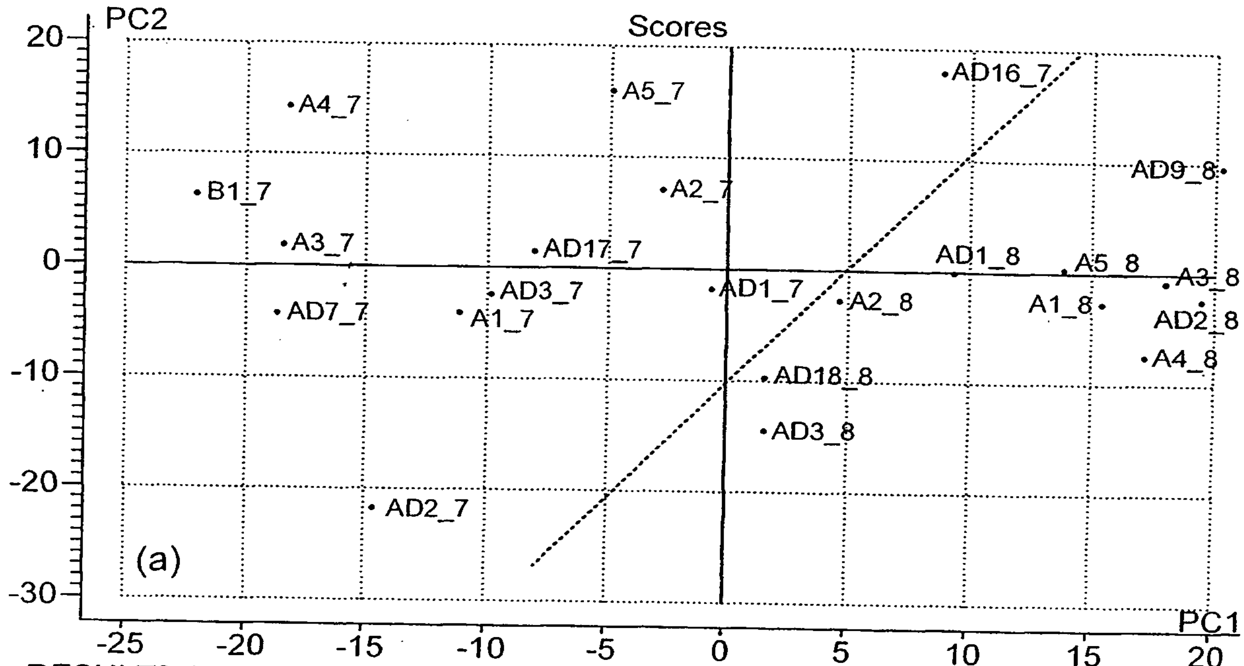
f) normalizing and standardizing said data set of step (e);

g) constructing a calibration model for classification, preferably using the statistical techniques Partial Least Squares Discriminant Analysis (PLS-DA) and Linear Discriminant Analysis (LDA);

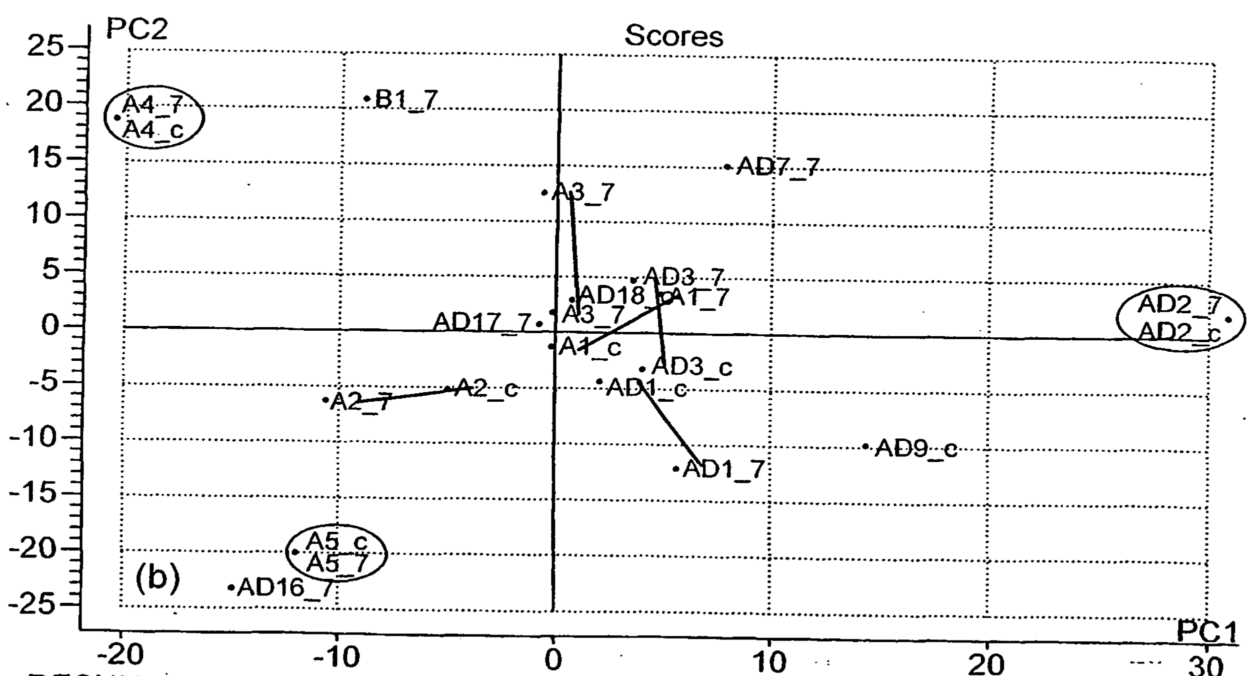
h) performing JackKnife analysis and identifying those oligonucleotide probes which are required for classification of said disease and normal samples into their respective groups.

FIG. 1

Effect of Direct Standardization (DS) on the Alzheimer Data measured in two different series of experiments

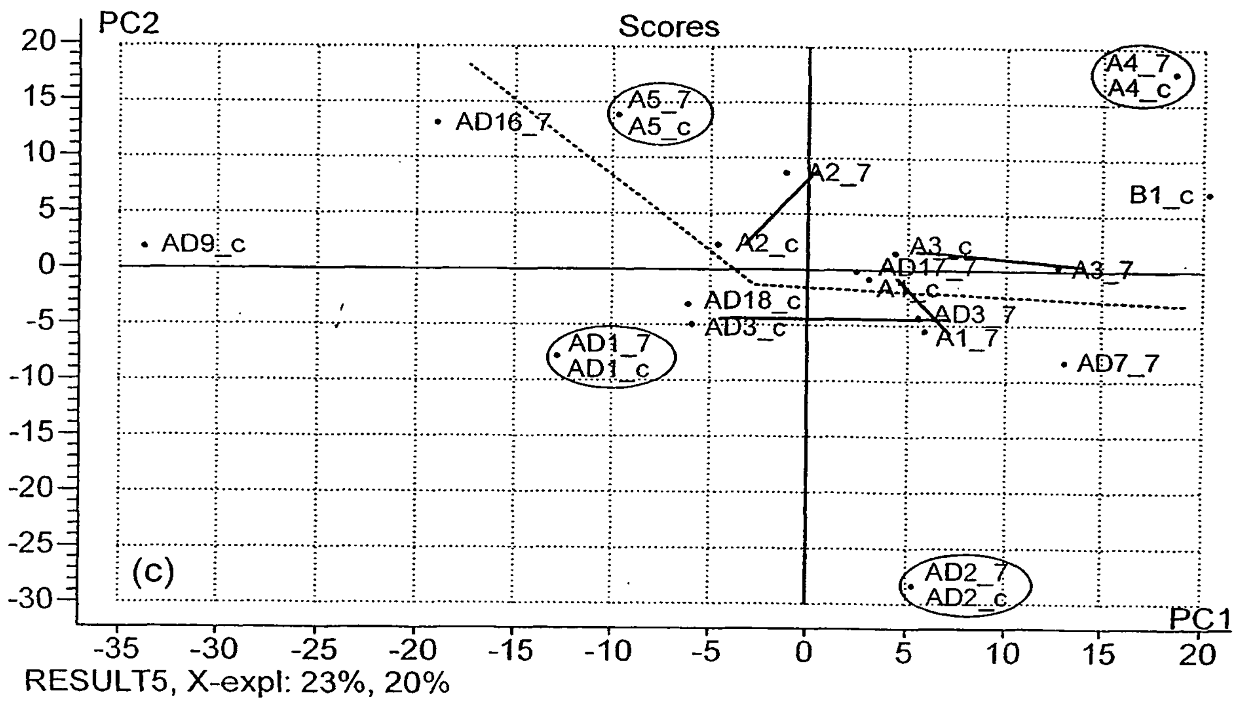


RESULT2, X-expl: 25%, 12%



RESULT1, X-expl: 24%, 20%

FIG. 1CONT'D


PC2
Scores
A4_7
A4_c
A5_7
A5_c
AD16_7
A2_7
B1_c
AD9_c
A2_c
A3_c
AD17_7
A3_7
A1_c
AD18_c
AD3_7
AD3_c
A1_7
AD1_7
AD1_c
AD7_7
AD2_7
AD2_c
(c)
PC1
20
15
10
5
0
-5
-10
-15
-20
-25
-30
-35
RESULT5, X-expl: 23%, 20%

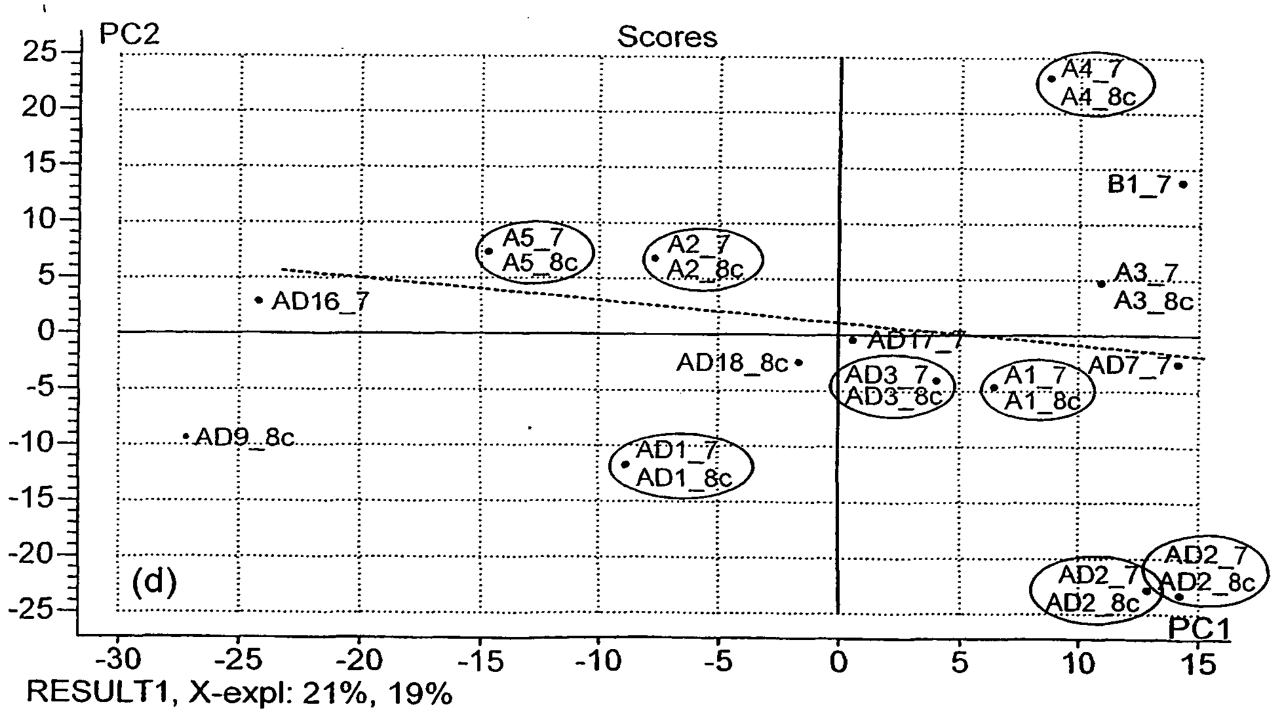

PC2
Scores
A4_7
A4_8c
B1_7
A5_7
A5_8c
A2_7
A2_8c
A3_7
A3_8c
AD16_7
AD17_7
AD18_8c
AD3_7
AD3_8c
A1_7
A1_8c
AD7_7
AD9_8c
AD1_7
AD1_8c
AD2_7
AD2_8c
(d)
PC1
25
20
15
10
5
0
-5
-10
-15
-20
-25
-30
RESULT1, X-expl: 21%, 19%

FIG. 2

Projection of normal (including benign) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 44 informative genes

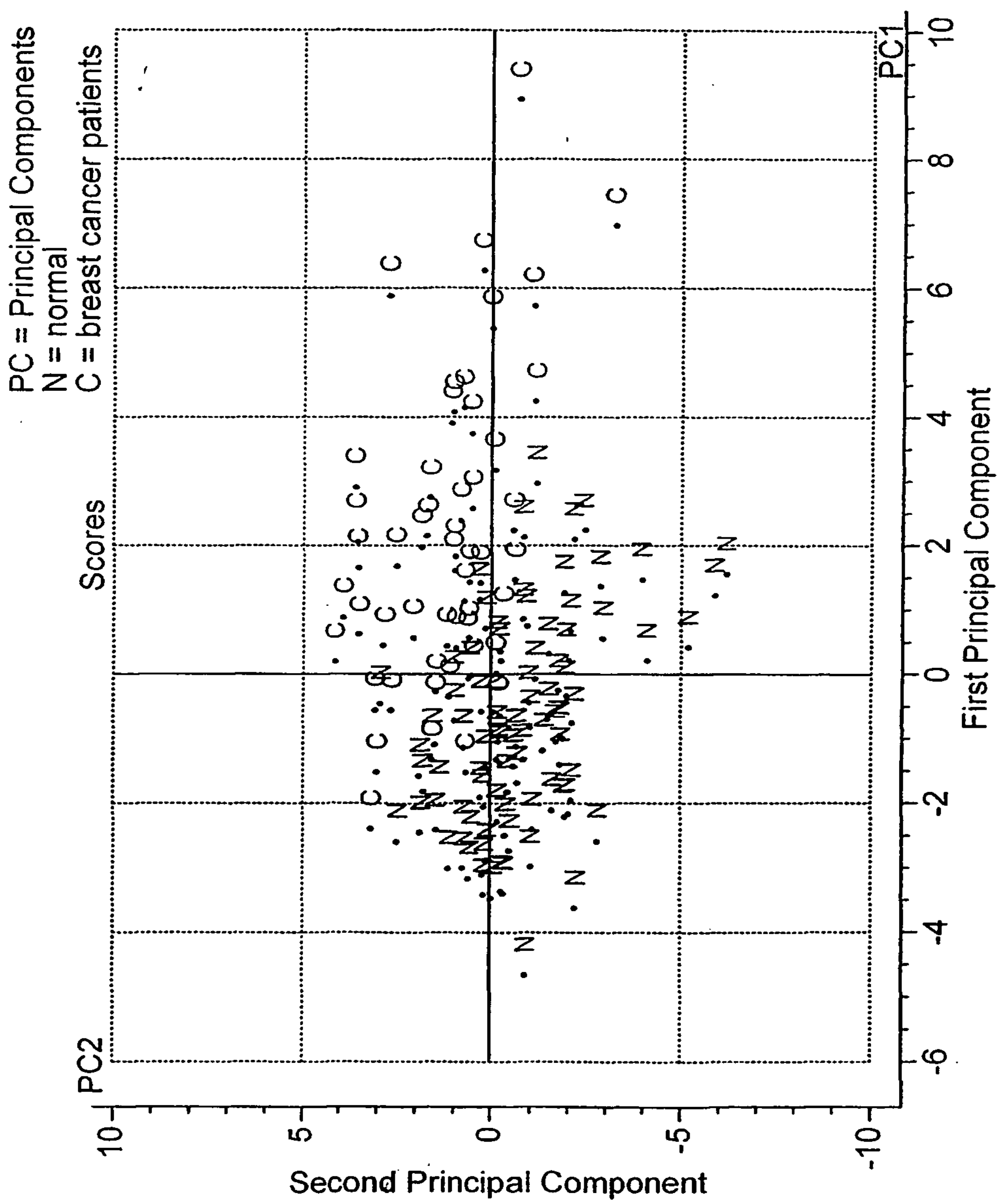


FIG. 3

Projection of individuals with and without Alzheimer's disease onto a classification model generated by PLSR-DA using 182 informative genes.

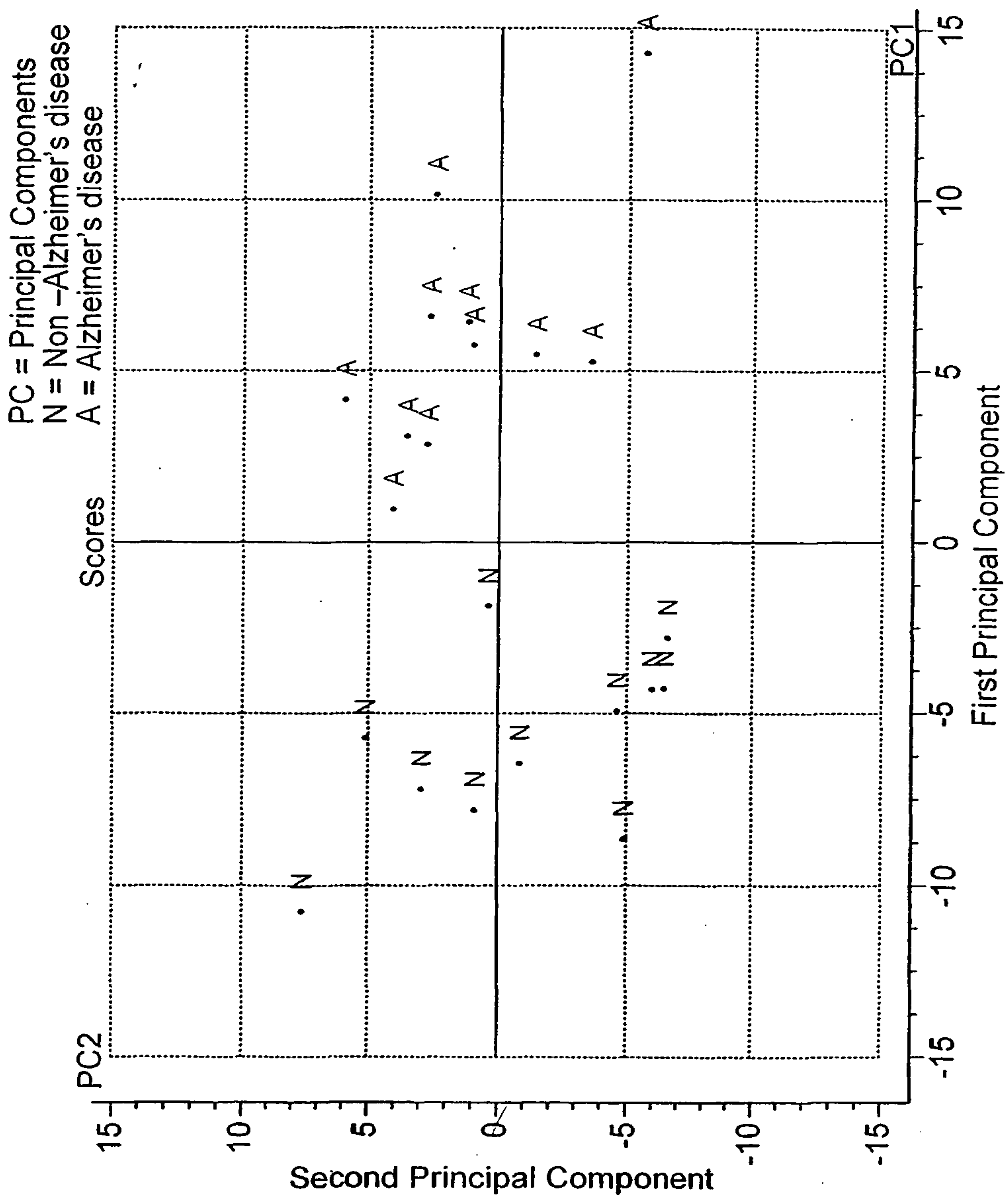


FIG. 4

Projection of normal (women with suspected mammogram but no breast cancer) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 719 cDNAs

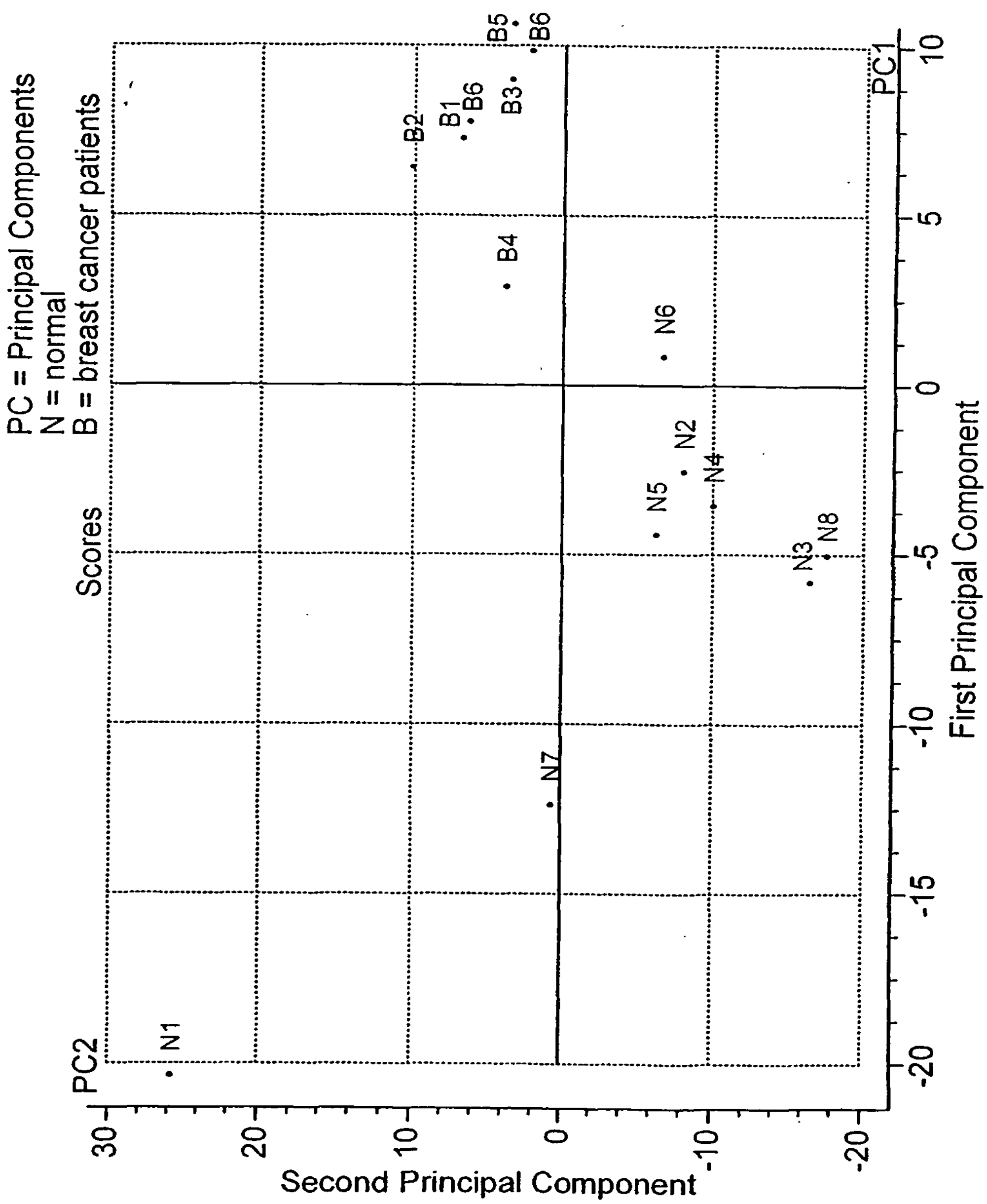


FIG. 5

Prediction of normal (women with suspected mammogram but no breast cancer) and breast cancer samples based on 3 principal components using the data of 719 cDNAs

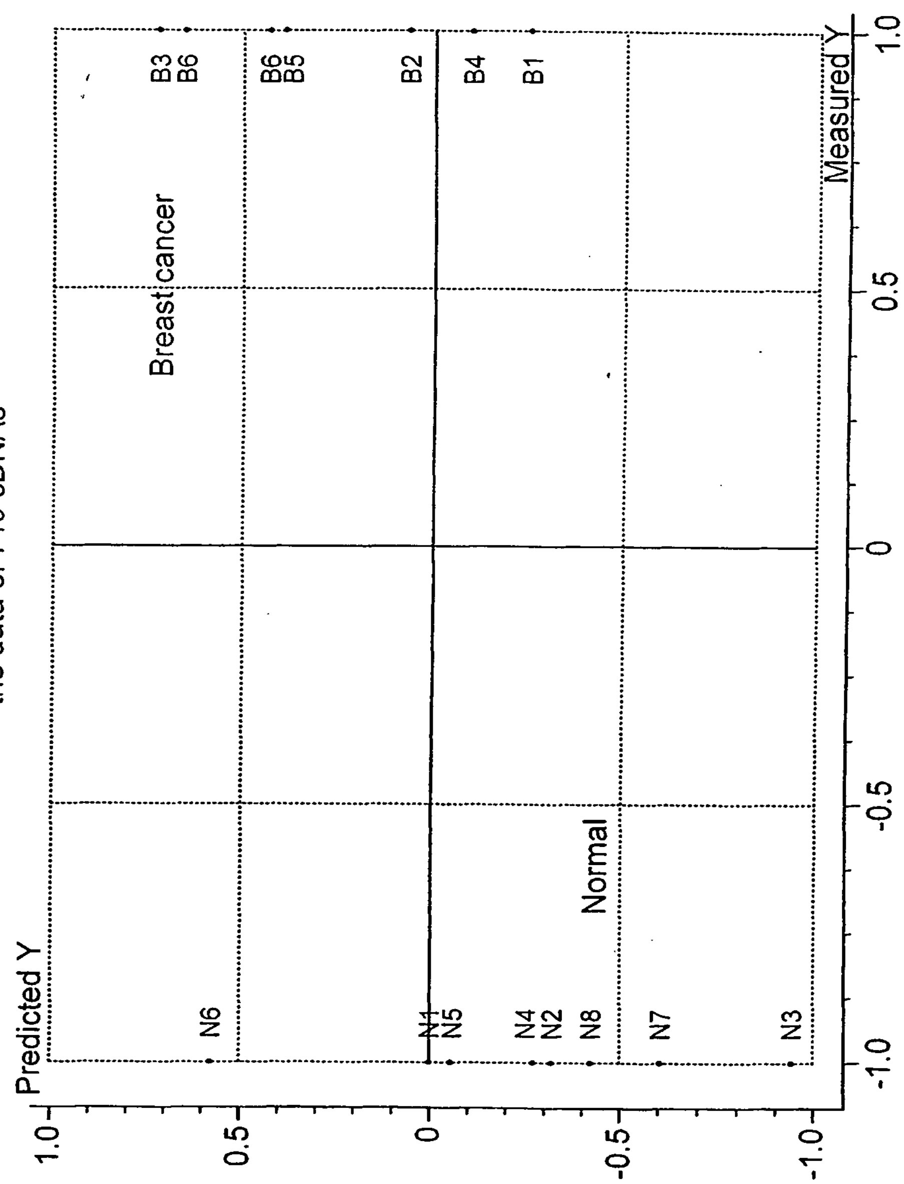


FIG. 6

Projection of normal (women with suspected mammogram but no breast cancer) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 111 cDNAs already on file

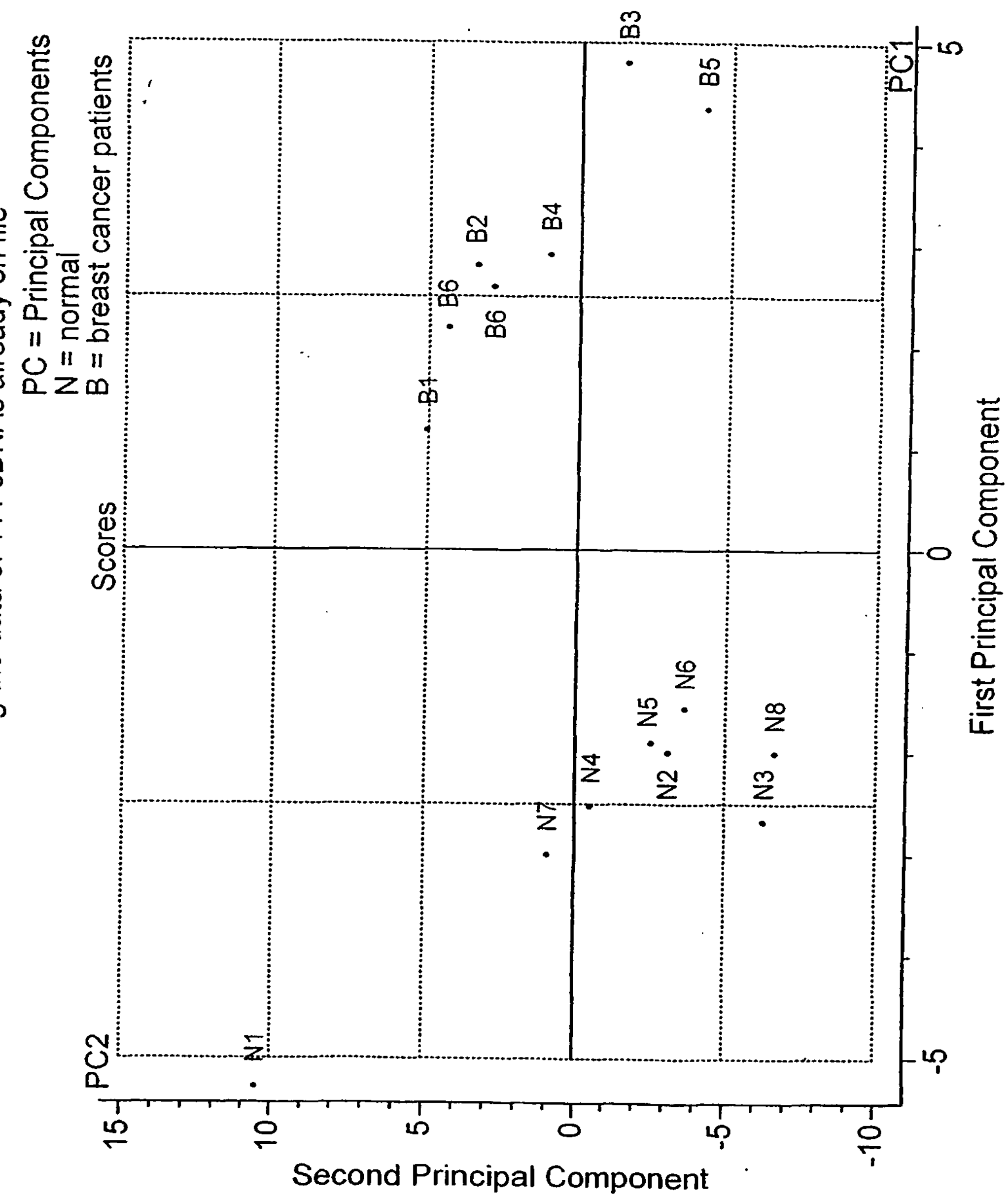


FIG. 7

Prediction of normal (women with suspected mammogram but no breast cancer) and breast cancer samples based on 4 principal components using the data of 111 cDNAs already on file

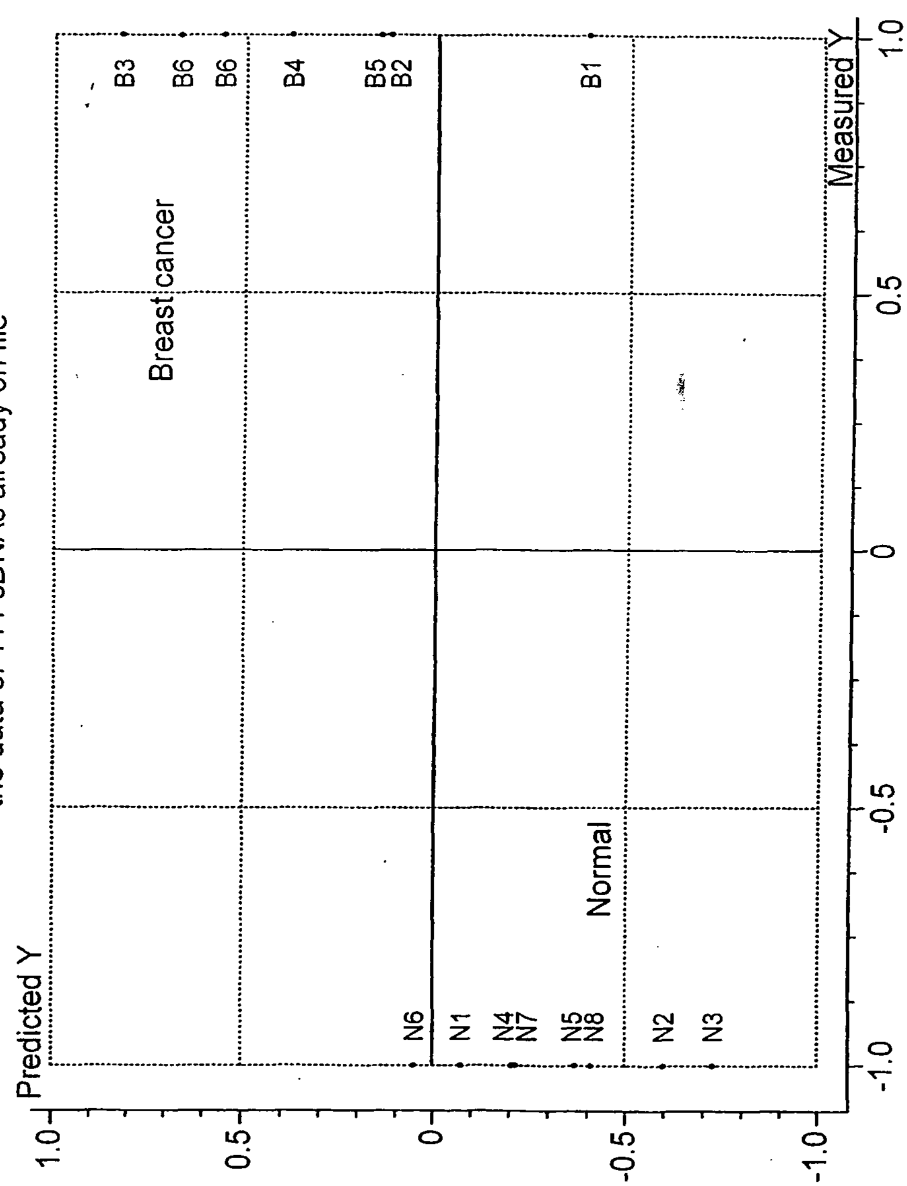


FIG. 8

Projection of normal (women with suspected mammogram but no breast cancer) and breast cancer samples onto a classification model generated by PLSR-DA using the data of 345 sequenced cDNAs for breast cancer

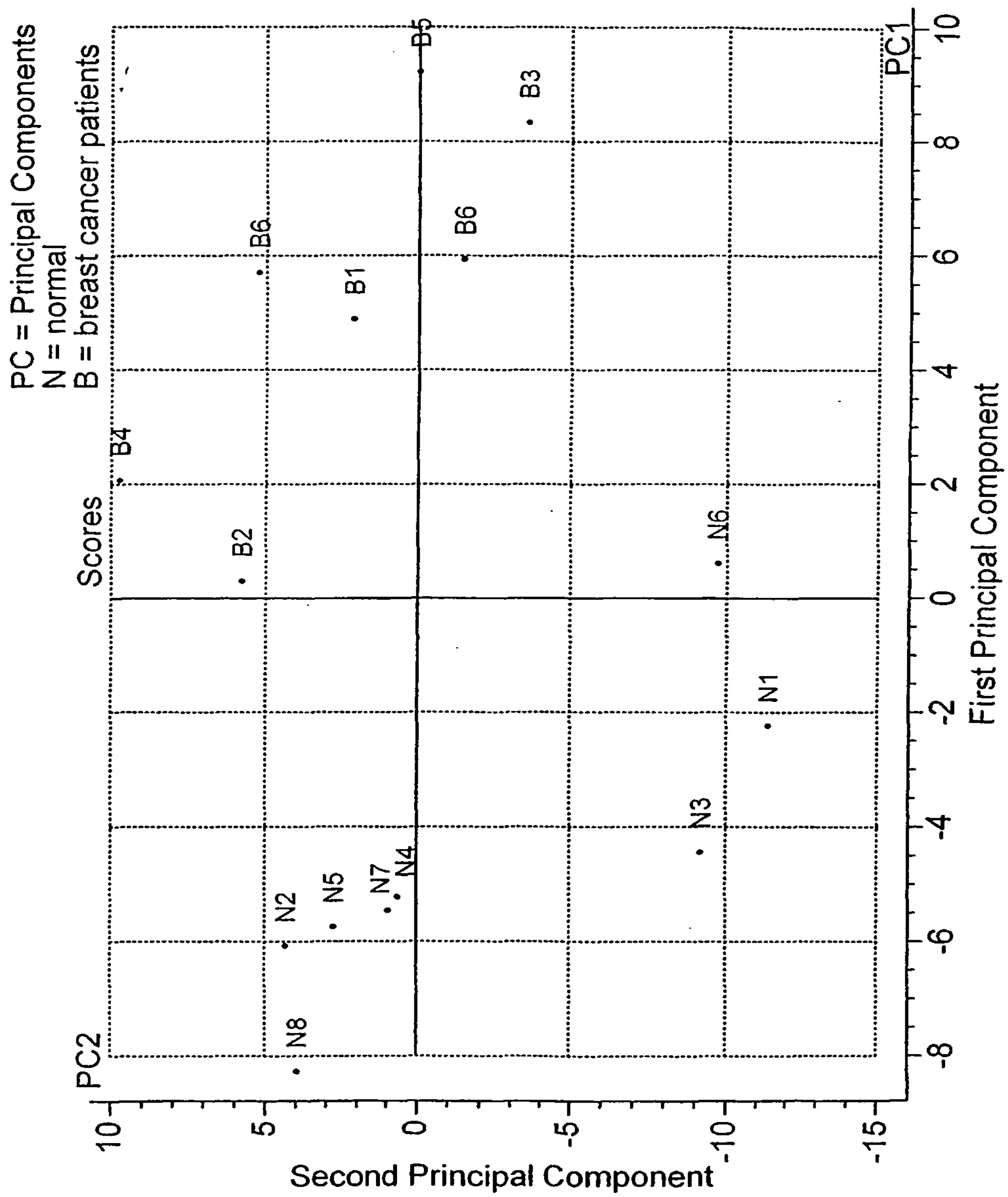


FIG. 9

Prediction of normal (women with suspected mammogram but no breast cancer) and breast cancer samples based on 3 principal components using the data of 345 sequenced cDNAs

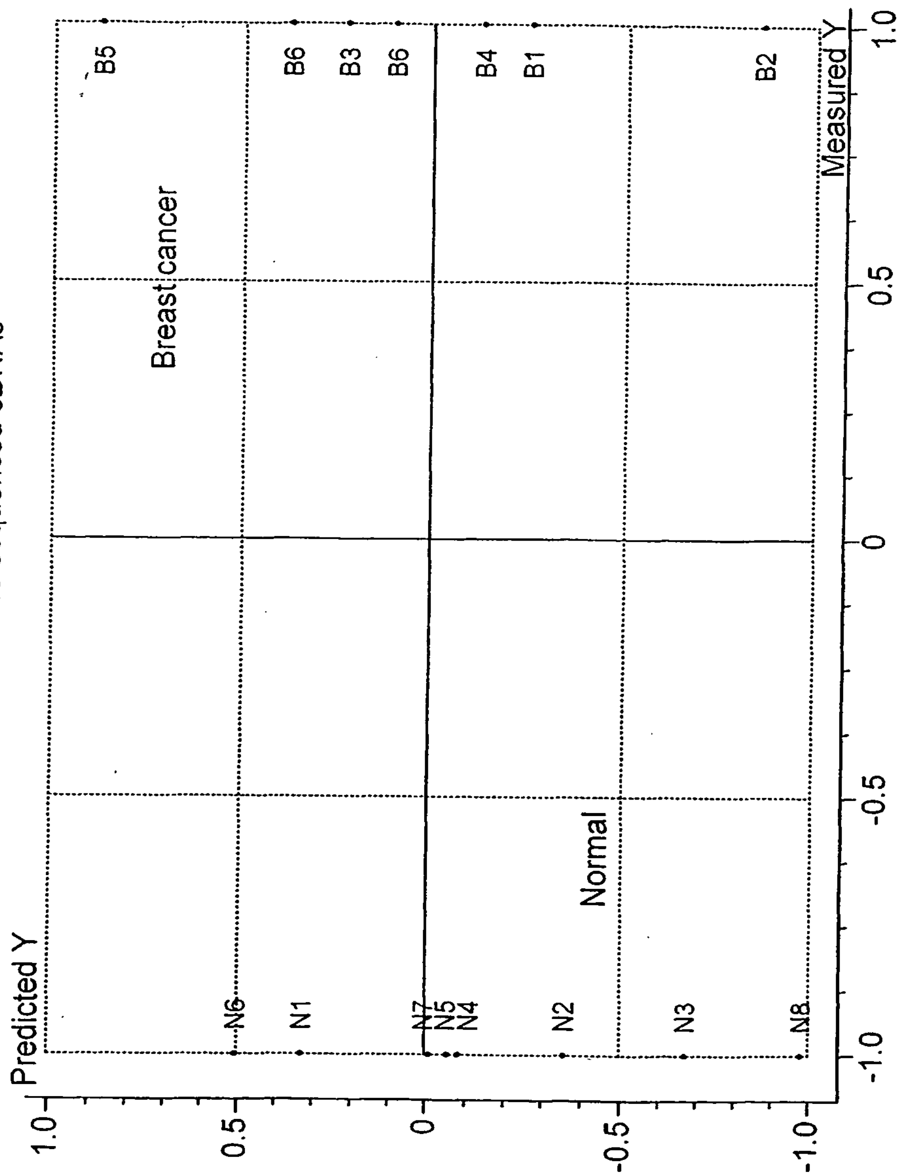


FIG. 10

Projection of non-alzheimer and alzheimer samples onto a classification model generated by PLSR-DA using the data of 520 sequenced cDNAs

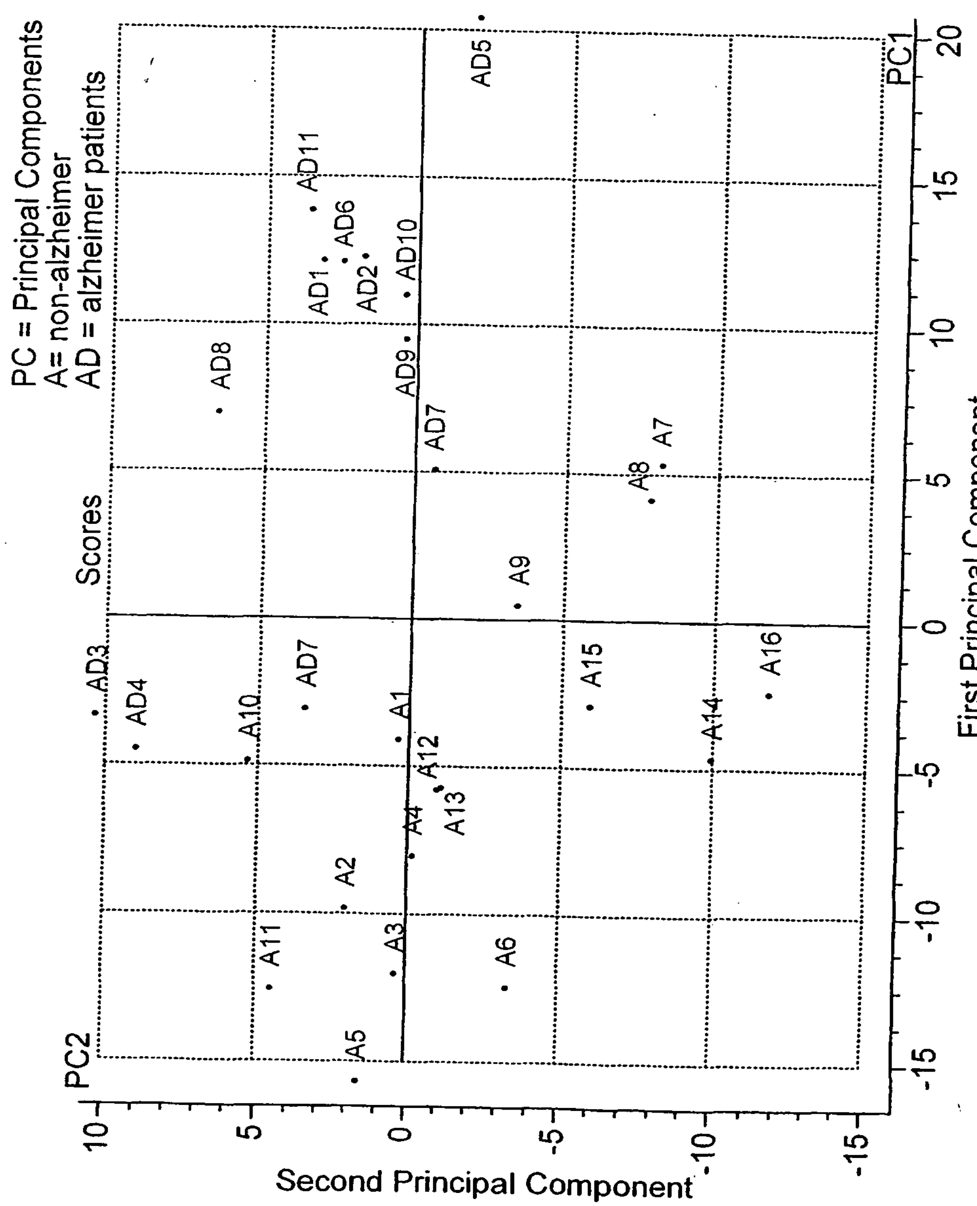


FIG. 11

Prediction of non-alzheimer and alzheimer samples based on 4 principal components using the data of sequenced cDNAs